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GenCore version 4.5
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OM protein - protein search, using sw model

July 10, 2002, 22:14:33 ; Search time 56.06 Seconds (without alignments) 462.792 Million cell updates/sec Run on:

US-09-823-676-2

Perfect score:

1 MELNRSEADEAKAETTPTGG......IYGMSGGSGGGGGATRPAF 270 Sequence:

BLOSUM62 Scoring table:

283138 seqs, 96089334 residues Gapop 10.0 , Gapext 0.5 Searched:

283138 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

prk_71:*
1: pirl:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SIIMMARTES

		æ			SUMMAKLES	
Result No.	Score	Query	Lengt	DB		Description
-		100.0	270		706118	3 + 0 × 8 - 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
8	706.5	50.8	311	(7	F86341	
e	646.5	46.4		7	C71448	hypothetical prote
4	645.5	46.4		7	Н96792	G
Ŋ	629.5	45.2	317	~	D84890	probable AT-book n
9	625.5		339	~	T06612	hypothetical prote
7	919	44.3	285	7	E84766	_
8	605	œ.	324	7	T04576	hypothetical prote
σ	581	41.7	265	7	T47898	
10	572	÷	310	N	147695	_
11	554	39.8	257	~	B84860	_
12	417	。	206	~	G86279	0
13	274	19.7	296	~	G84747	
14	255.5	е Э	334	~	T04572	hypothetical prote
15	246.5	ζ.	347	~	T06584	
91	243	Ľ.	439	N	T52291	
17	239.5	17.2	404	N	T05553	hypothetical prote
18	239	۲.	455	N	T05081	
19	227	· •	365	C	T06615	
070	225	16.2	348	C)	T02462	ᅩ
T 7	2.18 2.18	٠	345	~	T01348	hypothetical prote
77	2117		348	~	T47923	probable DNA-bindi
57.	162.5	٠,	574	~	A84782	hypothetical prote
4.1	146		405	7	T29167	
52	139		307	N	T27609	_
56	~;		694	~	86	_
27	135.5	6.7	290	~	341	_
82.0	♥ '		839	~	55	
67	131	9.4	388	7	T29173	

hypothetical alver	protein kinase soo	related to Nup98-N	mucin, submaxillar	hypothetical prote	hypothetical prote	female sterile hom	hypothetical prote	probable deoxyribo	gene mastermind pr	. CREB-binding prote	hypothetical alvei	regulatory factor	fibroin-3 related	insulin receptor s	hypothetical prote
E70806	S35327	T51890	T03099	T31611	A83412	A43742	D46449	S57795	T13998	T13828	H70589	A35913	T49510	S30185	B64924
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Length		Indels
OB 2;	e-85;	, 0
Score 1392; DB 2;	Pred. No. 6.66	; Mismatches
		ative 0
Query Match 100.0%	Best Local Similarity	Matches 270; Conserva

9 1 MELNRSEADEAKAETTPTGGATSSATASGSSSGRRPRGRPAGSKNKPKPFTITTRDSPNV

61 LRSHVLEVTSGSDISEAVSTYATRRGCGVCIISGTGAVTNVTIRQPAAPAGGGVITLHGR 120 ò

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121 FDILSLTGTALPPPAPPGAGGLTVYLAGGQGQVVGGNVAGSLIASGPVVLMAASFANAVY 180 엄 ο

DRLPIEBEBETPPPRITGVQQQQPEASQSSEVTGSGAQACESNLQGGNGGGGVAFYNLGMN 240 181 ò

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241 MNNFQFSGGDIYGMSGGSGGGGGATRPAF 270 δ

241 MNNFQFSGGDIYGMSGGSGGGGGATRPAF 270

hypothetical protein F9H16.12 - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Dec-2001 C;Accession: F86341 R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon

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43; Gaps

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Cyaccession: H96792

RiTheologis, A.; Excert, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon RiTheologis, A.; Excert, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon ansen, N.E.; Hughes, B.; Huizar, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, ansen, N.F.; Hughes, B.; Huizar, L.; Suon and the state of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                unknown protein F14G6.10 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar_2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               122 DILSLIGTALPPPAPPGAGGLTVYLAGGQGQVVGGNVAGSLIASGPVVLMAASFANAVYD 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             74 ISEAVSTYATRRGCGVCIISGTGAVTNVTIRQPAAPAGGGVITLHGRFDILSLTGTALPP 133
                                                                                                                                                                                                                                                                      134 PAPPGAGGLTVYLAGGQGQVVGGNVAGSLIASGPVVLMAASFANAVYDRLPIEEEETPPP 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     194 RITGVQQQQPEASQSSEVTGSGAQACESNLQGGN-----GGGGVAFYNLGMNMN-NF 244
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                                                                           19 GGATSSATASGSSS-----GRRPRGRPAGSKNKPKPPTIITRDSPNVLRSHVLEVTSGSD 73
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                                                                                                                                                                                                                                                                                                                                                                                                                          C; Superfamily: Arabidopsis thaliana hypothetical protein T12H17.200
   Matches 136; Conservative 32; Mismatches 47; Indels
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A;Molecule type: DNA
A;Residues: 1-302 <STO>
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Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719
A;Accession: F86341
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cross-references: GB:AE005172; NID:94836899; PIDN:AAD30602.1; GSPDB:GN00141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EVTSGSDISEAVSTYATRRGCGVCIISGTGAVTNVTIRQPAAP-----AGGGVITLHG 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       180 YDRLPIEEEETP------PPRTTGVQQQQPEASQSSEVTGSGAQACESNLQGGNG 228
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C;Superfamily: Arabidopsis thallana hypothetical protein T12H17.200
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C;Superfamily: Arabidopsis thaliana hypothetical protein 712H17.200
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Pred. No. 9.9e-36;
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C;Species: Arabidopsis thaliana (mouse-ear cress)
A;Variety: columbia
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A; Molecule type: DNA
A; Residues: 1-311 <STO>
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7;

Length 302; Indels

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11;
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                                                                                                                                                                                                                                                 141 GLTVYLAGGQGQVVGGNVAGSLIASGPVVL--------MAASFANAVYDRLPIE- 186
                                                                                                                                                                                                                                                                                                                                                                               179 AGOPPPPPPRIKLENP-LDYGSAWAAAAQCRYGDLASLHGGGAAGPGSGSPSTAASSS 237
                                                                                                                                             Gaps
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus.
                                                                                                                                                                         25 ATASGSSSG--RRPRGRPAGSKNKPKPPTIITRDSPNVLRSHV-LEVTSGSDISEAVSTY
                                                                                                                                                                                                    8 AATEGSSSGRARRPSGASTSSKDSYLGSTSVISDSAKELCKAVSVSLGLGVEALEHLSSG
                                                                                                                                                                                                                                                                                                                                                    187 EEETPPPRITGVQQQPEASQSSEVTGSGAQACESNLQGGNGGGGV------A
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MEDLINE-87280230; PubMed-3611111;
Eckhardt A.E., Timpte C.S., Abernethy J.L., Toumadje A.,
Johnson W.C. Jr., Hill R.L.;
"Structural properties of porcine submaxillary gland apomucin.";
J. Biol. Chem. 262:11339-11344(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Timpte C.S., Eckhardt A.E., Abernethy J.L., Hill R.L.;
Porcine submaxillard Alenda apomucin contains tandemly repeated,
identical sequences of 81 residues.";
J. Biol. Chem. 263:1081-1088(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUB-Submaxillary gland;
MEDLINE-91236743; PubMed-2033060;
Bckhardt A.E., Timpte C.S., Abernethy J.L., Zhao Y., Hill R.L.;
Porcine submaxillary mucin contains a cystine-rich,
carboxyl-terminal domain in addition to a highly repetitive,
glycosylated domain.";
                                                                                                                                             26;
                                                                                                             9.6%; Score 133; DB 1; Length 709; 24.6%; Pred. No. 0.15; tive 32; Mismatches 126; Indels
                                                                      40E7666137E97B6B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                            234 FYNLGMNMNNFQFSGGDIYGMSGGSGGGGGGA-----TRP 268
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-0CT-1989 (Rel. 12, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
 LIGAND-BINDING.
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                                           POLY-ALA.
POLY-GLY.
               POLY-GLN.
POLY-PRO.
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MEDLINE-88087170; PubMed-2826455;
                                                                        77391 MW;
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709 AA;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its way mon-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                             FESTIOUES.
-1- PTM: EXTENSIVELY O-LINKED GLYCOSYLATED ON SER AND THR RESIDUES OF THE REPEAT UNITS. HIGHEST GLYCOSYLATION APPEARS TO OCCUR ON SER RESIDUES WHICH HAVE GLY AT POSITIONS AT +2 OR -2 FROM THE GLYCOSYLATION SITE OR, WHERE GLY IS THE PENULTIMATE RESIDUE. THE PRESENCE OF PROLINE (USUALLY AT POSITION +3 OR -3) APPEARS TO ALSO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ENHANCE GLYCOSYLATION.
-!- SIMILARITY: CONTAINS 1 VWFC DOMAIN.
-!- SIMILARITY: CONTAINS 1 C-TERMINAL CYSTINE KNOT-LIKE DOMAIN (CTCK).
         Gerken T.A., Owens C.L., Pasumarthy M.;

"Determination of the site-specific O-glycosylation pattern of the porcine submaxillary mucin tandem repeat glycopeptide. Model proposed for the polypeptide:galnac transferase peptide binding site.";

"J. Biol. Chem. 272:9709-9719(1997).

-1- FUNCTION: APOMUCIN IS PART OF WICCIN, THE MAJOR GLYCOPROTEIN SYNTHESIZED AND SECRETED BY WICCOUS CELLS OF THE SUBMAXILLARY GLAND. ITS HIGHLY VISCOUS AQUEDUS SOLUTIONS SERVE TO LUBRICATE THE ORAL CAVITY AND TO PROTECT IT FROM THE EXTERNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (MUCIN TYPE).
                                                                                                                                                                                                                               -- SUBGNIT: INTERMOLECULAR DISULFIDE BONDS COULD HELP MAINTAIN A MULTIMERIC MUCIN STRUCTURE.
                                                                                                                                                                                                                                                                                                 -1- TISSUE SPECIFICITY: SUBMAXILLARY MUCOSAE.
-1- DOMAIN: CONTAINS TANDEMLY REPEATED, IDENTICAL SEQUENCES OF 81
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MEDLINE-97248516; PubMed-9092502;
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EMBL; M2174; AAA30998.1; --
EMBL; M2109; AA40090.1; --
InterPro; IPR001359; Cys_knot.
InterPro; IPR01007; VWFC.
InterPro; IPR01007; VWFC.
INTERPRO; IPR01007; VWFC.
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CARBOHYD

CARBOHYD

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OM protein - protein search, using sw model

July 10, 2002, 22:21:23 ; Search time 49.21 Seconds (without alignments) 212.442 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-09-823-676-2 1392 1 MELNRSEADEAKAETTPTGG.....IXGMSGGSGGGGGGATRPAF 270

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

105224 seqs, 38719550 residues Searched:

105224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	ANDR RABIT	DTG	DROME P13709	2_DROME P40791	922260	097952	270	097960 papio	097775	homo	00805	DROME	E	P22293	P08672	010637	Q9pjy2 chlan	_HUMAN Q12948	HUMAN Q10571 homo	O53553 mycob		MYCTU 053810				P15923	D54320 mile m	COM CACACA	COM CACACA	076743 cae	2AEEL 076743 cae	AEEL 076743 cmc 10MAN 099618 h n 10USE 095188 mus	AREL 076743 GROUNDAN 0995188 h nu 0905E 092188 mus 095188 h nu 000SE 09399 mus
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ALIGNMENTS

AA.	ue) Late) eceptor) (Fragment).	Oryctolagus cuniculus (Rabbit). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus. NCBI_TaxID=9986;	it androg it androg EIR RECEP RESSION A TARGET TI MODULATIN STEROLD-	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires alicense agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).	Lrecep. rec_lig. 1. EPTOR; 1. ation; DNA-binding; Nuclear protein; MODULATING. 4-TYPE.
709 AA	upda n upo	ıta; ridae	Prostate; M.J.; the rabbit ssues."; S AND THEIR GENE EXPRE TION IN TAR	It is nform e. Tong emove t (Section).	1. DNA-b
PRT;	33, Created) 33, Last sequence update) 39, Last annotation update) (Dihydrotestosterone receptor)	ıs (Rabbit). Chordata; Craniata; Veı Lagomorpha; Leporidae;	TISSUE-Prost McPhaul M.J. McPhaul M.J. ance of the r intal tissues); HORMONES ANI RRYOTIC GENE RRYOTIC GENE RRYOTIC GENE RRYOTIC GENE RREE DOMAINS: NUB A C-TERMI	is SWISS-PROT entry is copyright. It is p tween the Swiss Institute of Bioinformat e Buropean Bioinformatics Institute. The by non-profit institutions as long diffed and this statement is not removed. titles requires a license agreement (See send an email to license@isb-sib.ch).	66; AAC48469.1; 196; IGDC. 1PR00103; Androgen_recep. 1PR001628; zf-C4. 106; Androgen_recep; 1. 105; zf-C4; 1. 105; zf-C4; 1. 1059; znF_C4; 1. 1099; znF_C4; 1. 10039; znF_C4;
STANDARD;		is cuniculus (Ral Metazoa; Chorda Eutheria; Lagome	JUENCE FROM N.A. ALIN-NEW ZEALAND WHITE, TISSUE-P LINE-96044663; PubMed-7559153; nograd A., Wilson J.D., McPhaul oning and partial sequence of t ression in fetal urogenital tis Androl. 16:209-212(1995). FUNCTION: THE STEROID HORMONES THE REGILATION OF EUKARYOTIC G PROLIFERATION AND DIFFERENTIAT SUBCELLUTAR LOCATION: Nuclear. DOMAIN: COMPOSED OF THREE DOMA A DNA-BINDING DOMAIN AND A C-T SIMILARITY: BELONGS TO THE NUC NR3 SUBFAMILY:	entry is class Institutions of it institutions is statements a licens to licens	U16366; AAC48469.1; P05536; IGDC. rvo; IPR001103; Androgen. rvo; IPR001103; Hormone_rv PF02166; Androgen_recep; PF001104; hormone_rec; 1. PF00104; hormone_rec; 1. PF00105; Zf-C4; 1. SM0039; Zf-C4; 1. SM0039; Zf-C4; 1. E; PS00031; NUCLEAR_RECEI or; Transcription regulatinger; Steroid-binding. R 1 1 1 ND 349 414 N
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AESOLI ANDR_RABIT ID ANDR_RABIT AC P49699;	01-FEB-1996 (Rel. 01-FEB-1996 (Rel. 30-MAY-2000 (Rel. Androgen receptor AR OR NR3C4.	Oryctolagus cuni Eukaryota; Metaz Mammalia; Euther NCBI_TaxID=9986;	SEQUENCE FROM N.A. STRAIN-NEW ZEALAND WHITE; TISSUE-Prostate; MEDLINE-96044663; PubMed-7559153; Krongrad A., Wilson J.D., McPhaul M.J.; "Cloning and partial sequence of the rabbi expression in fetal urogenital tissues."; J. Androl. 16:209-212(1995). ITHE REGULATION OF EUKARYOTIC GENE EXPR PROLIFERATION AND DIFFERENTIATION IN TISSUECLUIAR LOCATION: Nuclear	This SWISS-PP between the the European use by non- modified and entities requ	MBL; U163 SSP; P065 SSP; P065 InterPro; InterPro; fam; PF002 fam; PF00 fam; PF00 fam; PF00 fam; PF00 Interpro; SM0 MART; SM0 Interpro; SM0 Int
ANDR_R ID A	OF DI	00 00 8	K K K K K K K K K K K K K K K K K K K	3888888888	DOR DOR DOR TTT TTT

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probable DNA-binding protein - garden pea
c;Species: Pisum sativum (garden pea)
c;Date: 23.Apr.1999 #sequence_revision 23.Apr.1999 #text_change 01-Dec-2000
c;Accession: T06584; T06582
F;Sato, N.; Kazuno, A.A.; Ohta, N.; Ohshima, K.
submitted to the EMBL Data Library, June 1996
A;Bescription: Identification of a novel family of DNA-binding proteins with two AT-hook
A;Reference number: 215774
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Best Local Similarity 36.7%; Pred. No. 2.8e-09;
Matches 61; Conservative 30; Mismatches 66; Indels
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A; Status: preliminary: translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Gassareferences: EMBL:X98738; PIDN:CAA67290.1
A; Cross references: EMBL:X98738; PIDN:CAA67290.1
A; Cross references: EMBL:X98738; PIDN:CAA67290.1
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-114, 'S', 116-334 <SA2>
A; Cross references: EMBL:X98739; PIDN:CAA67291.1
A; Experimental source: CV. Alaska
C; Keywords: DNA binding
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Search completed: July 10, 2002, 22:26:43 Job time: 730 sec

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Query Match 39.8%; Score 554; DB 2; Length 257; Best Local Similarity 52.8%; Pred. No. 1.1e-29; Matches 113; Conservative 30; Mismatches 37; Indels 34; Gaps 4;	C; Accession: G84747 R; Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujil, C.Y M.; Koo, H.; Moffat, K.S.; Cronin, I.A.; Shen, M.; Vanakon, S.P.; Fujil, C.Y
QY 16 TPTGGATSSATASGSSSGRRPRGRPAGSKNKPK 48	euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Umayam, L.; Tallon, Nature 402, 761-768, 1999 A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A:Reference number: A&4420.
Qy 49 PPTIITRDSPNVLRSHVLEVTSGSDISEAVSTYATRRGCGVCIISGTGAVTNVIIRQPAA 108 : :: : :: :	A; Accession: G84747 A; Status: preliminary A; Molecule type: DNA A; Residues: 1-366 / cmo.
Qy 109 PAGGGVITLHGREDILSLTGTALPPPAPPGAGGLTVYLAGGOGQVVGGNVAGSLLASGPV 168 : ::	A;Cross-references: GB:AE002093; NID:92459442; PIDN:AAB80677.1; GSPDB:GN00139 C;Genetics: At;Gene At;233520 A;Gene At;233520 A;Map Dosition: 2
169	Query Match Query Match Best Local Similarity 35.1%; Pred. No. 3.6e-11; Matches 87; Conservative 28; Mismatches 81; Indels 52; Gaps 11;
KESULT 12 (8657) F14L17.27 protein – Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress)	LEVTSGSDI 74 : : CTVLAGEDV 121
C;Date: U2-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 02-Nov-2001 C;Accession: G86279 C;Accession: G86279 C;Accession: G86279 C;Accession: G86279 C;Accession: G86279 C;Accession: G86279 C;Accession: C;Accession: G;Accession: G;Ac	OY 75 SEAVSTYATRRGCGVCIISGTGAVTNVTIRQPAAPAGGGVITLHGRPDILSLTGTALP 132
Kim,	OY 133 PPAPPG-AGGLTVYLAGGQGQVVGGNVAGSLIASGPVVLMAASFANAVYDRLPIEEEE 189
arzial Tallon	NGGGGVA GSVA
A. Meterence number: A86141; MUID:21016719 A. Accession: G86279 A. Status: preliminary A. Molecule type: DNA	
A; Mesidues: 1-206 <sto> A; Cross-references: GB: AE005172; NID: 97262692; PIDN: AAF43950.1; GSPDB: GN00141 A: Man nosition: 1</sto>	RESULT 14 1104572
Query Match Query Match Best Local Similarity 46.0%; Pred. No. 9.16-21; Matches 91, Conservative 32, Mismatches 59; Indels 16. Cans.	hypothetical protein T12H17.160 - Arabidopsis thaliana C.Species: Arabidopsis thaliana (mouse-ear cress) C.Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 14-May-1999 C.Accession: T04572 R.Bevan, M.; Hilbert, H.; Braun, M.; Holzer, E.; Brandt, A.; Duesterhoeft. A.; Rancro
AGSKNKPKPPTIITRDSPNVLRSHVLEVTSGSDISEAVSTYATRRGGGVCIISG 94 : : : : : : : : : : RGSKNKPKAPIFVTIDPPMSPYILEVPSGNOVDEALNRFCRGKALGFCVLSG 63	
OY 95 TGAVINVIIRQPAAPAGGGVITLHGRFDILSLTGTALPPPAPPGAGGLTVYLAGG 149	A. residues: 1.34 < LBL.) A.Cross-references: EMBL.AL021635 A. Experimental source: cultivar Columbia; BAC clone T12H17 C. Genetics:
OY 150 QGOVUGGNVAGSLIASGPUVLMAASFANAVYDRLPIEEEETPPPRTTGVQQQQPEASOSS 209 1 1 1 1 1 1 1 1 1	A; mar position: 44 A; Introns: 139/1; 161/3; 205/3 A; Note: T12H17.160
Oy 210 EVTGSGAQACESNLQGGN 227 Oy 11	Query Match 18.4%; Score 255.5; DB 2; Length 334; Best Local Similarity 27.5%; Pred. No. 6.8e-10; Matches 64; Conservative 38; Mismatches 68; Indels 63; Gaps 6;
RESULT 13 G84747	OY 17 PTGGATSSATASGSSGRRPRGRP
AT-hook DNA-binding protein (AHPI) [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Iste: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001	

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A;Gene: At2g42940
A;Map position: 2
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 | sequence_revision 20-Apr-2000 | #text_change 02-Sep-2000
C;Accession: T47898
R;Choisne, N.; Robert, C.; Brottier, P.; Wincker, P.; Cattolico, L.; Artiguenave, F.; Sa will the Cothe Protein Sequence Database, March 2000
A;Reference number: 224479
R;Bevan, M.; Hilbert, H.; Braun, M.; Holzer, E.; Brandt, A.; Duesterhoeft, A.; Bancroft, A;Bebrited to the Protein Sequence Database, February 1998
A;Reference number: 215377
A;Accession: T04576
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94 GTGAVTNVTIRQPAAPAGGGVITLHGRFDILSLTGTALPPPAPPGAGGLTVYLAGGQGQV 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----ETEREIDG 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            133 PPAPPGAGGLTVYLAGGQGQVVGGNVAGSLIASGPVVLMAASFANAVYDRLPIEEEE--T 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34 RRPRGRPAGSKNKPKPPTIITRDSPNVLRSHVLEVTSGSDISEAVSTYATRRGCGVCIIS 93
                                                                                                                                                                                                                                                                                                                                                                                       74 ISEAVSTYATRRGCGVCIISGTGAVTNVTIRQPAA-PAGGGVITLHGRFDILSLTGTALP 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                  19 GGATSSATASGSSG-----RRPRGRPAGSKNKPKPPTIITRDSPNVLRSHVLEVTSGSD 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30;
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A,Note: T4C21.280
C,Superfamily: Arabidopsis thaliana hypothetical protein T12H17.200
                                                                                                                                                                                                                                                                                                                                 30;
                                                                                                                                                                                           A;Map position: 4
A;Note: T12H17.200
C;Superfamily: Arabidopsis thaliana hypothetical protein T12H17.200
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                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 56.8%; Pred. No. 6e-33;
Matches 129; Conservative 26; Mismatches 42; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        57; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         191 P-----PPRTTGVQQQQPEASQSSEVTGSGAQACESNLQG 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 265 PVHGGGGGGSLESPPMMGQQLQHQQQAM----SGHQGLPPNLLG 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: EMBL:AL021635
A;Experimental source: cultivar Columbia; BAC clone T12H17
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Matches 119; Conservative 31; Mismatches
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A; Residues: 1-265 <CHO>
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                                                                                                 A; Molecule type: DNA
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R;Lib, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y. M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter Nature 402, 761-768, 1999
                                                                                                                                                                                                                                                                                                                                  hypothetical protein T22E16.220 - Arabidopsis thaliana C, Species: Arabidopsis thaliana (mouse-ear cress) (Species: Arabidopsis thaliana (mouse-ear cress) (Species: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Jun-2000 (Species: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Jun-2000 (Species: T47695 #terence number: Z4472 #terence number:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             237 PIEEEQ------QOEQPLOLEDGKKQKEENDDNESGNNGNEGSMQPPMYNMPPNFIP 287
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214 SGAQACESNLQGGNGGGGVAFYNLGMNMNNFQFSGGDIYGMSGGSGGGGGGTRPAF 270
                                                                                                         219 NAARAIGTOTOKOLMODATSFIGSPSNLINSVSLPGEAY------WGTORPSF 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Map position: 3
A;Note: T22E16.220
C;Superfamily; Arabidopsis thaliana hypothetical protein T12H17.200
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47.8%; Pred. No. 8.6e-31;
tive 44; Mismatches 69; Indels
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Best Local Similarity
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A; Residues: 1-257 <STO>
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Affille: Sequence and analysis of Chromosome 2 of the plant Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: DNA A;Residues: 1-285 <STO>A;Residues: 1-285 <STO>A;Cross-references: GB:AE002093; NID:g3668079; PIDN:AAC61811.1; GSPDB:GN00139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   probable AT-hook DNA-binding protein (imported) - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001
                                                                        64 HVLEVTSGSDISEAVSTYATRRGCGVCIISGTGAVTNVTIRQPAAPAGGGVITLHGRFDI 123
                                                                                                           88 NINSGSEGKEMSLHGGEGGSGGGGGGGGGQMIRRPRGRPAGSKNKPKAPIIITRDSANALRT 147
                                                                                                                                                                                          124 LSLTGTALPPPAPPGAGGLTVYLAGGQGQVVGGNVAGSLIASGPVVLMAASFANAVYDRL 183
                                                                                                                                                                                                                    PIEEEETPPPRTTGVQQQQPEASQSSEVTGSGAQACESNLQGGNGGGGVAFYNLGMNMNN 243
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C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jun-2000
C:Accession: T04576
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          127 TGTALPPPAPPGAGGLTVYLAGGQGQVVGGNVAGSLIASGPVVLMAASFANAVYDRLPIE 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              187 EEETPPPRITGVQQQQPEASQSSEVTGSGAQACESNLQGGGGGGVAFYNLGMNMNFQF 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             229 EHE--------BHLQSGGGGGGNYSEAT----GGGGGLPFFNLPMSMP01-- 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11 AKAETTPTGGATSSATASGSSSG----RRPRGRPAGSKNKPKPPTIITRDSPNVLRSHVL 66
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C;Superfamily: Arabidopsis thaliana hypothetical protein 712H17.200
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49.6%; Pred. No. 9.9e-34;
Live 30; Mismatches 64; Indels
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A;Accession: E84766
                                                                                                                                                                                                                                                                                                                                                       267 PLEEDEMQTP-----
                                                                                                                                                                                                                                                                                                                                                                                                              244 FQFSGGDIYGMSGGSGGGGG 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   247 SGGDIYGMSGGSGGGGGGATRP 268
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Best Local Similarity
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                                                                                                                                                                                                                                              Rilin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, L. euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein F16J13.120 - Arabidopsis thaliana
(SiSpecides: Arabidopsis thaliana (mouse-ear cress)
(SiSpecides: Arabidopsis thaliana (mouse-ear cress)
(SiSpecides: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 20-Jun-2000
(S.Accession: T06612
(S.Bevan, M.; Hilbert, H.; Braun, M.; Holzer, E.; Brandt, A.; Duesterhoeft, A.; Bancroft, A.; Reference number: 215789
(A. Reference number: 215789
(A. Residues: 1-339 CBEV)
(A. Residues: 1-339 CBEV)
(C. Sexperimental source: cultivar Columbia; BAC chone F16J13
(C. Genetics: A. RTEP: F16J13.120
(C. Genetics: A. RTEP: F16J13.120
(C. Superfamily: Arabidopsis thaliana hypothetical protein T12H17.200
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                                                                                                                                                                   C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60 VLRSHVLEVTSGSDISEAVSTYATRRGCGVCIISGTGAVTNVTIRQPAAPAGGG--VITL 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     118 HGRFDILSLIGTALPPPAPPGAGGLTVYLAGGQGQVVGGNVAGSLIASGPVVLMAASFAN 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            175 HGRFEILSLSGSFLPPPAPPAASGLTIYLAGGGGGVVGGSVVGPLMASGPVVIMAASFGN 234
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                                                                                                                             probable AT-hook DNA-binding protein [imported] - Arabidopsis thaliana C.Species: Arabidonsis thaliana
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C;Superfamily: Arabidopsis thaliana hypothetical protein T12H17.200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   178 AVYDRLPIEEEETPPPRTTGVQQQPEASQSSEVTGSGAQACESNLQGGNGGG 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               235 AAYERLPLEEDD------GEEQTAGAVANNIDGNATM------GGG 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2; Length 317;
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44.9%; Score 625.5; DB 2; Length 339;
Best Local Similarity 49.2%; Pred. No. 2.8e-34;
Matches 129; Conservative 28; Mismatches 48; Indels 57
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265 AGQGQLRGNMSGYDQFAGDPH-LLGWGAAAAAPPRPAF 302
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Best Local Similarity 54.1%; Pred. No. 1.4e-34;
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                                                                                                                                                                                                                                                                                                                                                                                             A; Reference number: A84420; MUID: 20083487
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A;Molecule type: DNA
A;Residues: 1-317 <STO>
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                                                                                                                          GENERAL INFORMATION:
APPLICANT: VAN HEERDE, GEORGE V.
APPLICANT: VAN HEERDE, GEORGE V.
APPLICANT: VAN HEERDE, GEORGE V.
APPLICANT: WONGSTRA, JAN B.
APPLICANT: MOOBROEK, ANDREAS
APPLICANT: WEREN, MADREAS
APPLICANT: WIND, RICHELE D.
APPLICANT: WIND, RICHELE D.
APPLICANT: WIND, RICHELE D.
TITLE OF INVENTION: SULVER HALIDE EWULSIONS WITH RECOMBINANT COLLAGEN
TITLE OF INVENTION: SULVER HALIDE EWULSIONS WITH RECOMBINANT COLLAGEN
TITLE OF INVENTION: SULVER HALIDE EWULSIONS WITH RECOMBINANT COLLAGEN
TITLE OF INVENTION: SULVER HALIDE EWULSIONS
TITLE OF INVENTION: PREPARATION THEREOF
FILE REFERENCE: 2728-2
CURRENT FILING DATE: 1998-12-23
CURRENT FILING DATE: 1998-12-23
SOFTWARE: PALENTIN VET. 2.1
SEQ ID NOS: 50
SOFTWARE: PALENTIN VET. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Description of Artificial Sequence: Synthetic COTHER INFORMATION: amino acid sequence US-09-219-849-50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 7.3%; Score 101.5; DB 4; Length 595; Best Local Similarity 23.4%; Pred. No. 0.74; Matches 71; Conservative 19; Mismatches 118; Indels 95
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Patent No. 6150081
GENERAL INFORMATION:
APPLICANT: VAN HEERDE, GEORGE V.
APPLICANT: VAN RIJN, ALEXIS C.
APPLICANT: BOUWSTRA, JAN B.
APPLICANT: DE WOLF, FREDERIK A.
APPLICANT: MOOBROEK, ANDREAS
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                                                                                      Sequence 50, Application US/09219849 Patent No. 6150081
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APPLICANT:
APPLICANT:
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                         APPLICANT: VAND DEN BOSCH, TANJA J.
TITLE OF INVENTION: SILVER HALIDE EMULSIONS WITH RECOMBINANT COLLAGEN
TITLE OF INVENTION: SILVER HALIDE EMULSIONS WITH RECOMBINANT COLLAGEN
TITLE OF INVENTION: BY SUITABLE FOR PHOTOGRAPHIC APPLICATION AND ALSO THE
TITLE OF INVENTION: PREPARATION THEREOF
FILE REFERENCE: 2728-2
CURRENT APPLICATION NUMBER: US/09/219,849
CURRENT FILING DATE: 1998-112-23
NUMBER OF SEQ ID NOS: 50
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 49
LENGTH: 822
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                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Description of Artificial Sequence: Synthetic US-09-219-849-49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 7.3%; Score 101.5; DB 4; Length 822; Best Local Similarity 23.4%; Pred. No. 1.1; Matches 71; Conservative 19; Mismatches 118; Indels 95,
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Job time: 2810 sec
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WIND, RICHELE D.
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TYPE: PRT
ORGANISM: Artificial Sequence
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US-09-219-849-48
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1425 AAHGHGAHRVRQGPERVLGGHGVPDVRQRRGHAAGDEGAVAV-GRVDPALAELVEALVGG 1483
                                                                                                                  1484 LHPRVLQPGHGLAGGPAVDEAHEGLVLLPRVPHLRDEDGHGPGRGAVAGRGLADVVLVPE 1543
                                                                                                                                                                                                                                       167 PVV-LMAASFANAVYDR-----LPIEEEETPPPRTTGVQQQQPEASQSSEVTGSGAQA 218
                                                            130 ALPPPAPPG---AGGLTVYLA----------GGQGQVVGGNVAGSLIASG 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         68 VTSGSDISEAVSTYATRRGCGVCI -- ISGTGAVTNVTIRQPAAPAGGGVITLHGRFDILS 125
                                                                                                                                                                                                                                                                                                                        219 CESNLQGGNGGGG-----VAFYNLGMNMNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7.4%; Score 103; DB 1; Length 760;
23.6%; Pred. No. 0.76;
tive 28; Mismatches 107; Indels 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Bonini, Nancy M.
APPLICANT: Belserson, William M.
APPLICANT: Belserson, William M.
APPLICANT: Belserson, William M.
TITLE OF INVENTION: PROGRAMMED CELL DEATH ANTAGONIST
TITLE OF INVENTION: PROGRAMMED
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/195,152
FILING DATE: 14-FEB-1994
CLASSIFICATION: 435
ATORNEY/AGENT INFORMATION:
NAME: Trecartin, Richard F.
REFERENCE/DOCKET NUMBER: 31,801
REFERENCE/DOCKET NUMBER: 31,801
FELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19 GGATSSATASGSSSGRRPRGRPAGSKNKPKPPTIITRDS--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1658 ---GGRGRGGRGGRGGGRAPR 1677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/08195152
Patent No. 5679541
                                                                                                                                                                                                                                                                                                                                                                                                                                                        245 OFSGGDIYGMSGGSGGGGGATR 267
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TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : 760 amino acids
amino acid
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Best Local Similarity
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APPLICANT: MOOBROEK, ANDREAS
APPLICANT: WERNEYN, WARC W.T.
APPLICANT: WIND, RICHELE D.
APPLICANT: VAN DEN BOSCH, TANJA J.
TITLE OF INVENTION: SILVER HALIDE EMULSIONS WITH RECOMBINANT COLLAGEN
TITLE OF INVENTION: PREPARATION THEREOF
                                                                                                                                                                                                                            149 ATASSFAQSAGSSFSTYQQAGGTSGGVSGEDGV-----VGGATVMSHWTHDGTG 197
                                                           126 LTGTALPPPAPPGAGGLTVYLAGGOGOVVGGNVAGSLIASGPV-----VLMAASFAN 177
                                                                                                                      198 SSAAVKSESRSPG----QVHASLDNGSVAGSNLYGCSSASNPLDGGAVAVNSSAVAAAAA 253
                                                                                                                                                                                        178 AVYD-----RLPIEEEETPPP------RTTGVQQQPE----ASQSSEVTGSGAQ 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        92 SGLDGAKGDAGPAGPKGEPGSPGENGAPGQMGPRGLP-GERGRPGPP------- 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64 HVLEVTSGSDISEAVSTYATRRGCGVCIISGTGAVTNVTIRQPAAPAG-GGVITLHGRFD 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         138 ------PTGPPGFPGAVGAAGPPGPTG-----PTGPPGFPGAVGAKGEAG 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       123 ILSLIGTALP-----PPAPPGAGGLTVYLAGGQGQVVGGNVAGSLIASG-PVVLMAASFA 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         214 SGAQACESNL----QGGNGGGGVAFYNLGMNMNNFQFSGGDIYGMSGGSG-GGGGGAT 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6 SEADEAKAETTPTG--GATSSATASGSSSGRRPRGRPAGSKNKPKPPTITTRDSPNVLRS 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ------PRTTGVQQQPEASQSSEVTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTHER INFORMATION: Description of Artificial Sequence: Synthetic; OTHER INFORMATION: amino acid sequence OTHER 1089-489-48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7.3%; Score 101.5; DB 4; Length 595; 23.4%; Pred. No. 0.74; Live 19; Mismatches 118; Indels 95
                                                                                                                                                                                                                                                                                                                  218 ACESNLQ------GGNGGGGVAFYN 236
                                                                                                                                                                                                                                                                                                                                                                              314 SGNNNSQLYSSPYAGYNNFGQQDYGG--YYN 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/219,849
CURRENT FILING DATE: 1998-12-23
NUMBER OF SEQ ID NOS: 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Patent No. blocco.;
GENERAL INFORMATION:
APPLICANT: VAN HEERDE, GEORGE V.
FAPPLICANT: VAN RIJN, ALEXIS C.
APPLICANT: BOUWSTRA, JAN B.
SAPLICANT: DE WOLF, FREDERIK A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 48, Application US/09219849 Patent No. 6150081
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1305 LPLGRAGPGDRVAEREQRGGHLLEAGGPEGGRGAGGRGQPERAGQQALEDAAAGQDAGVR 1364
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                                                ...-----MVPPTGSPG-GGLP---ADTAAQLTSAGR 344
                                                                                                                                                                                                                                                                                                             218 ACESNIQGGNGGGGVAFYNLGMNMNNFQ----FSGGDIYGM----SGGSGGGGGATRP 268
                                                                                                                                                                                                                                                                                                                                            Query Match 7.5%; Score 104; DB 1; Length 1958;
Best Local Similarity 20.6%; Pred. No. 2.1;
Matches 79; Conservative 36; Mismatches 142; Indels 126; Gaps
                                                                                                                99 TNVTIRQPAAPAGGGVITLHGRFDILSLTGTALPPPAPPGAGGLTVYLAGGQGQVV-GGN 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MELNRSEADEAKAETTPTGGATSSATASGSSSGRRPRGRPAGSKNKPKPPTIITRDS-PN 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60 VLRSHVLEVTSGSDISEAVSTYATRR--GCGV----------CIIS 93
                    45 NKPKPPTIITRDSP-----NVLRSHVLEVTSGSDISEAVSTYATRRGCGVCIISGTGAV 98
                                                                                                                                                                                                               158 VAGSLIASGPVVLMAASFANAVYDRLPIEEEETPPPRTTGVQQQQPEASQSSEVTGSGAQ
                                                                                                                                                                                                                                                               345 EAAAL--SGDVAVKAASL--------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pseudorabies Virus Deletion Mutants
Involving The EPO and LLT Genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Curtis P. Ribando
STREET: 1815 No. 5352596th University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/07/945,283
FILING DATE: 19920911
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Ribando, Curtis P
REGISTRATION NUMBER: 27976
TELECOMUNICATION INFORMATION:
TELEPHONE: 309-685-4011 ext.513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/07945283 Patent No. 5352596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Andrew K.
Ronald D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 19920911
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 1958 amino acids TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 309-685-4128
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Cheung, Andrew APPLICANT: Wesley, Ronal TITLE OF INVENTION: PSEUTITE OF INVENTION: INVO NUMBER OF SEQUENCE: 7
CORRESPONDENCE ADDRESS: 7
                                                                                                                                                                 315 ----MPAAP-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein
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CITY: Peoria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: US
ZIP: 61604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-07-945-283-2
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Best Local Similarity 22.9%; Pred. No. 0.22;
Matches 55; Conservative 15; Mismatches 54; Indels 116; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                               193 PRTTGVQQQQPEASQSSEVTGSGAQACESNLQGGNGGGGVAFYNLGMNMNNFQFSGGDIY 252
                                                                                                                                                                                                                    627 GGAGGSGGAGGSGGAGGSGGVGGSGG-----TTITED------LDITIDGA 672
                                                                                                                                                                                                                                                                    73 DISEAVSTYATRRGCGVCIISGTGAVTNVTIRQPAAPAGGGVITLHGRFDILSLTGTALP 132
                                                                                                                                                                                                                                                                                                                DGPITISEELTISGAGG---SGPGG------7AGPGGVG-------701
                                                                                                                                                                                                                                                                                                                                                                133 PPAPPGAGGLTVYLAGGQGQVVGGNVAGSLIASGPVVLMAASFANAVYDRLPIEEEETPP 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             737 PGGVGPGGYGPGGSGSGGV-GPGGYG-----PGGSGG----FYGPGGSEGPYGPSG--TY 784
                                                                                                                        Gaps
                                                                                                                                                                   19 GGATSSATASGS----SSGRRPRGRPAGSKNKPKPPTIITRDSPNVLRSHVLEVT-SGS 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: OF INVENTION: COMPOUNDS AND METHODS FOR THE PREVENTION AND NUMBER OF SEQUENCES: 241
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                     88;
                                                                     Length 907;
                                                                     Query Match 7.7%; Score 107; DB 2; Length 907
Best Local Similarity 26.2%; Pred. No. 0.44;
Matches 66; Conservative 13; Mismatches 85; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
EILLOATION NUMBER: US/09/056,556
FILING DATE: 07-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY AGENT INFORMATION:
NAME: MAKI, David J.
REGISTATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.457
TELECOMMUNICATION INFORMATION:
TELEPHOR: (206) 622-400
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 184:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 184, Application US/09056556 Patent No. 6350456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 460 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              785 GSGGYGPGGAG 796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                253 GMSGGSGGGGG 264
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seattle
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US-09-056-556-184
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US-09-010-928B-4
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                                                                                                                                                                                                                                                                                                                       542 GAGAGAGGYGGOGGYGAGARAGAAAAAGAGGAAGYSRGGRAGAAG-AGAGAAAGAGAG 600
                                                                                                                                                                                                                                                                                                                                                               139 AGGLTVYLAGGQGQVVGGNVAGSLIASGPVVLMAASFANAVYDRLPIEEEETPPPRTTGV 198
                                                                                                                                                                                                                                              ---- AGAAAGAGAGAAA 541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    635 GAGAGAAAGAGAAAGAGAGGYGGQGGYGAGAGAAAAAGAGAGRGGYGRGAGAGGYGGQ 694
                                                                                                                                                                Gaps
                                                                                                                                                                                                  19 GGATSSATASGSSSGRRPRGRPAGSKNKPKPPTIITRDSPNVLRSHVLEVTSGSDISEAV
                                                                                                                                                                                                                                                                                                                                                                                                                                              199 QQQQPEASQSSEVTGSGAQACESNLQGGNGGGGVAFYNLGMNMNNFQFSGGDIYGMSGGS
                                                                                                                                                                48;
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Patent No. 5756677
GENERAL INFORMATION:
APPLICANT: Lewis, Randolph V.
TITLE OF INVENTION: CDNAs Encoding Minor Ampullate Spider
TITLE OF INVENTION: Silk Proteins
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Birch, Stewart, Kolasch & Birch
STREET: PO. BOX 747
CITY: Falls Church
                                                                                                                  Query Match 7.9%; Score 110; DB 1; Length 832; Best Local Similarity 24.7%; Pred. No. 0.22; Matches 61; Conservative 14; Mismatches 124; Indels
                                                                                                                                                                                                                                                                                                                                                                                                  601 AGGY-----GGQGGYGAGAGAAAAAG-----AGSGGAGGYGR---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 22040-3487
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPREATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/458,298 FILING DATE: 02-07N-1995 CLASSIFICATION: 530 PRIOR APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: US 08/209,747 FILING DATE: 14-NAR-1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1447-104P
                                                                                                                                                                                                                                        503 GAGAGAAAAGAGAGGAGYGRGAGAG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Murphy Jr., Gerald M. REGISTRATION NUMBER: 28,977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 14
TELECOMMUNICATION INFORMATION
TELEPHONE: 703-205-8000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 832 amino acids
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS: single TOPOLOGY: linear
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                                       1..309
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US-08-209-747-2
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US-08-458-298-2
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      199 QQQQPEASQSSEVTGSGAQACESNLQGGNGGGGVAFYNLGMNMNNFQFSGGDIYGMSGGS 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19 GGATSSATASGSSSGRRPRGRPAGSKNKPKPPTIITRDSPNVLRSHVLEVTSGSDISEAV 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Lewis, Randolph V
APPLICANT: Lewis, Randolph V
APPLICANT: Hayashi, Cheryl Y
TITLE OF INVENTION: EXTREMELY ELASTIC SPIDER SILK PROFEIN AND DNA
TITLE OF INVENTION: CODING THEREFOR
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           601 AGGY -----GGQGGYGAGAGAAAAAG----AGSGGAGGYGR------
                                                                                                                                                                                                                                                                                                              48;
                                                                                                                                                                                                                                                                 ; DB 1; Length 832; 0.22;
                                                                                                                                                                                                                                                                                                              Indels
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                                                                                                                                                                                                                                                                                                            14; Mismatches 124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEE: BIRCH, STEWART, KOLASCH & BIRCH: 8110 GATEHOUSE RD. SUITE 500E FALLS CHURCH
                                                                                                                                                                                                                                                                   7.9%; Score 110;
                                                                                                                                                                                                                                                                                          Pred. No.
                                                                                      ORGANISM: N. clavipes
TISSUE TYPE: minor ampullate gland
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/09/010,928B FILLING DATE: 22-JAN-1998 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1447-109P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: VIRGINIA COUNTRY: UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 22042
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4, Application US/09010928B Patent No. 5994099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Murphy Jr., Gerald M REGISTRATION NUMBER: 28977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : 907 amino acids
amino acid
                                                                                                                                                                                                                                                                                                            61; Conservative
                                               internal
    protein
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                                                                                                                                                                                                                                                                                        Best Local Similarity
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                                                                  ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          259 GGGGGGA 265
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                                               FRAGMENT TYPE:
MOLECULE TYPE: HYPOTHETICAL:
                                                                                                                                                   ; NAME/KEY:
; LOCATION:
US-08-458-298-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-010-928B-4
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TOPOLOGY:
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                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                          Matches
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142 LTVYLAGGQGQVVG-GNVAGSLIASGPVVLMAASFANAVYDRLPIEEEETPPPRTTGVQQ 200
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                                                                                                                                                                                                                                                                           441 GGGNGGGNGGGGGGGGGGGGGGGGGG------GGALAAALAAAGAGG 492
                                                                                                                                                                                                                                                                                                                                                                89 VCII-----SGTGAVTNVTIRQPAAPAGGGVITLHGRFDILSLTGTALPPP-APPGAGG 141
                         Gaps
                                                                                                                                                      37 ---RGRPAGSKNKPKPPTIITR----DSPNVLRSHVLEVTSGSDISEAVSTYATRRGCG 88
                                                                 ---ATSSATASGSSSGRRP---- 36
                       90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Lewis, Randolph V.
APPLICANT: Colgin, Mark
APPLICANT: Colgin, Mark
APPLICANT: Colgin, Mark
TITLE OF INVENTION: Silk Proteins
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Birch, Stewart, Kolasch & Birch
STREET: P.O. Box 747
CITY: Falls Church
STATE: Virginia
Best Local Similarity 24.3%; Pred. No. 0.12;
Matches 75; Conservative 26; Mismatches 118; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/209,747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: N. Clavipes
TISSUE TYPE: minor ampullate gland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Murphy Jr., Gerald M.
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 1447-104P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 14-MAR-1994
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIE: 22040-3487
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/08209747
Patent No. 5733771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-205-8000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 703-205-8050 INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      832 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        261 GGGGATRPA 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                575 GFGGGSSAA 583
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TITLE OF INVENTION: NOVEL POLYPEPTIDE GENE CDNA, VECTOR
TITLE OF INVENTION: CONTAINING SAID CDNA, HOST CELLS TRANSFORMED WITH SAID
TITLE OF INVENTION: VECTOR, POLYPEPTIDE PRODUCED THEREBY, METHOD OF PRODUCING
TITLE OF INVENTION: SAID POLYPEPTIDE
TITLE OF INVENTION: TO SAID POLYPEPTIDE
                                                                                                                                                                                                                                   189 ETPPPRITGVQQ-----QQPEASQSSEVTGSGAQACESNLQGGNGGGGVAFYNL-GMNM 241
                                                                                                                                                                                                                                                                             345 -- APPLALGAYSPGQSSLYSSPCSQTSSAGSSGGGGGGGAGAGGAGGAGTYHCNLQAMSL 402
                                                                                                ------LSLDGADSAPPAPS 298
                                                                                                                                            138 G-----AGGLTV----YLAGGQGQVVGGNVAGSLIASGPVVLMAASFANAVYDRLPIEEE 188
                                                                                                                                                                                    299 APPPHHSQGFSVDNIMTSLRGSPQSAAAELSSGLLASA----AASSRAGI----- 344
           198 GRQPPPAPPEQADGNAPGPQPPPVRIQDIKTENGTCPSPPQPLSPAAALGSGS--AAAVP 255
                                                        80 TYATRRGCGVCIISGTGAVTNVTIRQPAAPAGGGVITLHGRFDILSLTG--TALPPPAPP 137
                                                                                                                                                                                                                                                                                                                                                                  403 YAAGERGCHLQGAPGGAGGSAVDNPLPDYSLPPVTSSSSSSLSHGGGG 450
                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MB storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM Compatible
OPERATING SYSTEM: Microsoft Windows 95
SOFTWARE: Word Perfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/O8/864,038A
PRIOR APPLICATION NUMBER: US/O8/864,038A
PRIOR APPLICATION DATA:
APPLICATION NUMBER: J997
FILING DATE: 15-July-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: From 1 to 738 DENTIFICATION METHOD: E (by experiment)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3, Application US/08864038A Patent No. 6001592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: C. Bruce Hamburg
REGISTATION NUMBER: 22,389
REPERENCE/DOCKEI NUMBER: F-561
TELECOMMUNICATION INPORMATION:
TELEPHONE: (212)965-7733
INPORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                  256 KIESPDSSSSSLSSGSSPPGSLPSARP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pinctada fucata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                812-5 Hirano
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CITY: Tsu-city
STATE: Mie-prefecture
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein
ORIGINAL SOURCE:
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CORRESPONDENCE ADDRESS:
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514-01
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APPLICANT: Kunio
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DB 3; Length 738;

8.0%; Score 112;

Query Match

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946 ATWQESGGVELGRIGPAPPGSATVCRPTRSVPNSRGDYMTMQIGCPRQSYVDTSPVA--P 1003
                                                                                                                                                                                                                                                110 AGGGVIT------LHGRFDILSLTGTALPP----------------- 133
                                                                                               886 KSPGEYVNIEFGSGQPGYLAGPATSRSSPSVRCPPQLHPAPREETGSEEYMNMDLGPGRR 945
                                                                                                                                     134 -------PAPPGAGGL---TVYLAGGQGQVVG---GNVAGSLIASGPVVLMA 172
                                                                                                                                                                                                                   173 ASFANAVYDRLPIEEEETPPPRTTG-VQQQQPEASQSSEVTGSGA---QACESNLQGG-N 227
                                                                                                                                                                                                                                                                                                     228 GGGGV-AFYNLGMNMNNFQ-----GG 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Sheffield, Val C.
APPLICANT: Sheffield, Val C.
APPLICANT: Stone, Edwin M.
APPLICANT: Stone, Edwin M.
APPLICANT: Nishimura, Darryl
APPLICANT: Patil, Shiva
TITLE OF INVENTION: CONGENITAL HEART DISEASE BASED ON A NOVEL HUMAN
TITLE OF INVENTION: TRANSCRIPTION FACTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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One Post Office Square
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FILING DATE: 22-MAY-1998
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Patent No. 6087107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Arnold, Beth E.
REGISTRATION NUMBER: 35,430
REFERENCE/DOCKET NUMBER: UIA-
TELECOMUNICATION INFORMATION:
TELEPHONE: 617-832-1000
TELEPHONE: 617-832-7000
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MEDIUM TYPE: Floppy disk
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amino acid
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; MOLECULE TYPE: protein US-09-083-351-2
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ZIP: 02109-2170
                                                                                                                                                                                                                                                                                                                                                                                   258 SGGGGGGAT 266
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Gaps

91;

Query Match
8.2%; Score 113.5; DB 3; Length 553;
Best Local Similarity 23.3%; Pred. No. 0.064;
Mutches ,67; Conservative 26; Mismatches 104; Indels 91

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12;
                                           198 GROPPPAPPEOADGNAPGPOPPVRIQDIKTENGTCPSPPOPLSPAAALGSGS--AAAVP 255
                                                                                                                                  256 KIESPDSSSSSLSSGSSPPGSLPSARP-----LSLDGADSAPPPAPS 298
                                                                                                                                                                                138 G----AGGLIV----YLAGGQGQVVGGNVAGSLIASGPVVLMAASFANAVYDRLPIEEE 188
                                                                                                                                                                                                                                                                                                                       345 -- APPLALGAYSPGOSSLYSSPCSQTSSAGSSGGGGGGGAGAAGGAGGAGTYHCNLQAMSL 402
                                                                                      80 TYATRRGCGVCIISGTGAVTNVTIRQPAAPAGGGVITLHGRFDILSLTG--TALPPPAPP 137
                                                                                                                                                                                                                              299 APPPHHSQGFSVDNIMISLRGSPQSAAAELSSGLLASA----AASSRAGI----344
                                                                                                                                                                                                                                                                            189 ETPPPRITGVQQ-----QQPEASQSSEVIGSGAQACESNLQGGNGGGGVAFYNL-GMNM 241
GRRPRGRPA----GSKNKPKPPTIITRD-----SPNVLRSHVLEVTSGSDISEAVS 79
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APPLICANT: Sheffield, Val C.
APPLICANT: Alward, Wallace L.M.
APPLICANT: Alward, Wallace L.M.
APPLICANT: Stone, Edwin M.
APPLICANT: Nishinura, Darryl
APPLICANT: Patil, Shiva
TITLE OF INVENTION: GLAUCOMA THERAPEUTICS AND DIAGNOSTICS
TITLE OF INVENTION: BASED ON A NOVEL HUMAN TRANSCRIPTION FACTOR
CORRESPONDENCE ADDRESS:
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ttive 26; Mismatches 104; Indels
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APPLICATION NUMBER: US/09/083,352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    UIA-029.01
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STREET: One Post Office Square
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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; Patent No. 6207450
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NAME: Arnold, Beth E.
REGISTRATION NUMBER: 35,430
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 617-832-7000 INFORMATION FOR SEQ ID NO: 2:
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ZIP: 02109-2170
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DD 886 KSPGEYVNIEFGSGQPGYLAGPATSRSSPSVRCPPQLHPAPREETGSEEVMNMDLGPGRR 945	Qy 134PAPPGAGGLTYYLAGGGCQVVGGNVAGSLIASGPVVLMA 172 1 1 1 1 1 1 1 1 1	Qy 173 ASFANAVYDRLPIEEEETPPPRTTG-VQQQQPEASQSSEVTGSGAQACESNLQGG-N 227	Oy 228 GGGGV-AFYNLGMNNNNFQ	Oy 258 SGGGGGAT 266 Db 1121 SGGGGGGS 1129	RESULT 3 PCT-US95-13041-15 ; Sequence 15, Application PC/TUS9513041 ; GENERAL INFORMATION: ; APPLICANT: WHITE, Morris F.	APPLICANT: SIN, Xiao Jian ; APPLICANT: PIERCE, Jacalyn H. ; TITLE OF INVENTION: THE IRS FAMILY OF GENES ; NUMBER OF SEQUENCES: 63	CORRESPONDENCE AUDRESS: CORRESPONDENCE AUDRESS: STREET: SAFET: Street, Suite 510	STATE: Bassachusetts COUNTRY: USA 2IP: 02109-1875	COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM FO Compatible OPERATING SYSTEM: PC-DOS ANS-DOS	SOFTWARE: ASCII text CURRENT APPLICATION DATA: APPLICATION NUMBER: PCT/US95/13041	SE F	ALIGNMENTAGES INFORMATION: REGISTRATION NUMBER: 35,965 REFERENCE/DOCKET NUMBER: JDP-022PC REFERENCE/DOCKET NUMBER: JDP-022PC	TELEPHONE: (617)227-7400 TELEFAX: (617)227-5941 INFORMATION FOR SEQ ID NO: 15: SEQUENCE CHARATERISTICS:	; LENGIH: 1124 amilio acids ; TYPE: amilio acid cid ; MOLECULE TYPE: peptide ; PERAMENT TYPE: peptide		Query Match 8.4%; Score 116.5; DB 5; Length 1234; Best Local Similarity 22.8%; Pred. No. 0.1; Matches 84; Conservative 29; Mismatches 125; Indels 131; Gaps	Qy 5 RSEADEAKAETTPTGGATSSATASGSSSGRRPRGRPAGSKNKPKPPTIITRDSPNVLRSH 64 :	Qy 65 VLEVTSGSDISEAVSTYATRRGCGVCIISGTGAVTNVTIRQPAAP 109
QY 59 NVLRSHV-LEVTSGSDISEAVSTYATRG-CGVCIISGTGAVTNVTIRQPAAPAGGGVIT 116 1 1 1 1 1 1 1	117 LHGRFDILSLTGTALPPPAPPGAGGLTVYLAGGQGQVVGGNVAGSLIASGPVVL		DD 34Z INSCALDEAMAYGENDITNFFLALAGPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPP	SULT 2 -08-317-310A-15 Sequence 15. Application 18/08317310A	Morris F. So Jian Jacalyn H.	; TITLE OF INVENTION: THE IRS FAMILY OF GENES ; NUMBER OF SEQUENCES: 64 ; CORRESPONDENCE ADDRESS: ; ADDRESSEE: LAHIVE & COCKFIELD	SIREET: 28 State Sireet CITY: Boston STATE: Massachusetts COUNTRY: ISA	: ZIP: 02109 ; COMPUTER READABLE FORM: ; MEDIUM TYPE: Floppy disk	COMPUTER: IBM PC compatible COMPUTER: IBM PC-DOS/MS-DOS SOFTWARE: ASCII text CURRENT APPLICATION DATA:	APPLICATION NUMBER: US/08/317,310A FILING DATE: 03-OCT-1994 CLASSIFICATION: 435 APPROPRIEM TANDOMATON.	; AIGNEL FOULS MYGES; ; REGISTRATION NUMBER: 35,965 ; REFERENCE POOCHER: JUMBER: JDP-022	TELEFORMORICATION: TELEFORMORICATION: TELEFAX: (617)227-5941 INFORMATION FOR SEQ ID NO: 15: SEGUENCE CHARACTERISTICS:	LENGTH: 1234 amino acids TYPE: amino acids TOPOLOGY: linear MOLECULE TYPE: peptide	TO CETUAL	z, benyen 5; Indels	Qy 5 RSEADEAKAETTPTGGATSSATASGSSSGRRPRGSRVRCKPPTIITRDSPNVLRSH 64	QY 65 VLEVTSGSDISEAVSTYATRRGCGVCIISGTGAVTNVTIRQPAAP 109	Qy 110 AGGCVIT1HGRFDILSLTGTALPP133

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16;
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FILING DATE:
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                                                              July 10, 2002, 21:34:28; Search time 46.14 Seconds (without alignments) 142.933 Million cell updates/sec
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Sequence 2, Appli
Sequence 2, Appli
Sequence 48, Appl
Sequence 50, Appl
Sequence 49, Appl
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Sequence 2, Appli
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Sequence 15,
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                                                                                                           1392
1 MELNRSBADEAKAETTPTGG......IYGMSGGSGGGGGATRPAF
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Sequence 6
Sequence 6
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Copyright (c) 1993 - 2000
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Patent No. 6235872

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Bredesen, Dale E.

APPLICANT: Rablaadeh, Sharroz

TITLE OF INVENTION: Polypeptides and Methods of Use

TITLE OF INVENTION: Polypeptides and Methods of Use

TITLE OF SEQUENCES: 72

CORRESPONDENCE ADDRESS:

ADDRESSEE: Campbell & Flores LLP

STREET: 4370 La Jolla Village Drive, Suite 700

CITY: San Diego

STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
COFTWARE: PatentIn Release #1.0, Version #1.25
APPLICATION NUMBER: US/09/041,886
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US-09-100-664A-3

US-09-100-664A-4

US-08-407-509B-94

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US-08-407-509B-94

US-08-407-791A-94

US-08-104-290-7

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US-08-105-237-46

US-09-026-587-4

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US-09-026-587-4

US-09-026-684-2

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CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cartryn A.
REFERENCE/DOCKET NUMBER: 9-LJ 2626
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEPHONE: (619) 535-9001
TELEPHONE: (619) 535-901
TELEPHONE: (619) 535-901
TELEPHONE: (619) 535-901
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LENGTH: 918 amino acids
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Search completed: July 10, 2002, 22:20:18 Job time: 3611 sec

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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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294 nghqmaqhdvy 304
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14-MAY-1999;
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18-MAY-1999;
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22-JUN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                  44; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAG21495 standard; Protein; 316 AA
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990S-0161404.
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nghqmaqhdvy 303
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PR 22.7UL-1999; 99US-014519.

PR 27.7UL-1999; 99US-014519.

PR 27.7UL-1999; 99US-014526.

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47.8%; Pred. No. 2.1e-38;
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Best Local Similarity 47.8%
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nghqmaqhdvy 298
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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Matches 120; Conservative 44; Mismatches 69;
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 Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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47.8%; Pred. No. 1.8e-38;
Live 44; Mismatches 69; Indels 1
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99US-0161993.
99US-0162142.
99US-0148684.
99US-0149178.
99US-0149175.
99US-0149722.
99US-0149723.
99US-0149929.
99US-0149930.
99US-0149930.
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Best Local Similarity 47.8%
Matches 120; Conservative
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26-OCT-1999;
28-OCT-1999;
28-OCT-1999;
29-OCT-1999;
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13-0CT-1999)
14-0CT-1999)
14-0CT-1999)
14-0CT-1999)
14-0CT-1999)
18-0CT-1999)
21-0CT-1999;
21-0CT-1999;
21-0CT-1999;
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21-0CT-1999;
22-0CT-1999;
22-0CT-1999;
13-AUG-1999;
117-AUG-1999;
18-AUG-1999;
20-AUG-1999;
20-AUG-1999;
23-AUG-1999;
23-AUG-1999;
25-AUG-1999;
27-AUG-1999;
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33-AUG-1999;
34-AUG-1999;
36-AUG-1999;
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Gaps

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The patent relates to polynucleotides encoding 35 plant transcription factors which may be used to modify phenotype associated with a plant's sugar sensing characteristics and increasing yield when their expression evel is altered. Sugars are central regulatory molecules that control aspects of physiology, metabolism and development. Therefore the CDNAs and proteins of the invention are useful for modifying the growth and espiration, starch and sucrose synthesis and degradation, pathogen response, wounding response, cell cycle regulation, pigmentation.

C feaponse, wounding response, cell cycle regulation, pigmentation, relationships in seeds, tubers, roots, and other storage organs leading to an increase in yield. The transcription factor polynucleotides and collypeptides may be used to alter the structure and developmental characteristics of plants such as sugarcane, turf, banana, blackberry, cice, oilseed, sunflower, alfalfa, sugarcane, turf, banana, blackberry, coffee, cucumber, eggplant, grapes, honey dew, lettuce, mango, melon, cohon, papaya, peas, peppers, pineapple, spinach, squash, sweet corn, cobacco, tomato, watermelon, rosaceous fruits and/or vegetable brassicas.

The present sequence is a homolog of Arabidopsis thaliana transcription
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M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                124 LSLTGTALPPPAPPGAGGLTVYLAGGQQQVVGGNVAGSLIASGPVVLMAASFANAVYDRL 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               184 PIEEEETPPPRITGVQQQPEASQSSEVIGSGAQACESNLQGGNGGGGVAFYNLGMNNN 243
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                                                                                                                                                                                                                                                                                             Heard J, Pineda O, Pilgrim M, Adam L, Riechmann JL;
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                                                                                                                       MENDEL BIOTECHNOLOGY INC.
                                                  17-NOV-1999; 99US-0166228.
17-APR-2000; 2000US-0197899.
22-AUG-2000; 2000US-0227439.
                  14-NOV-2000; 2000WO-US31414.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 49.2
Matches 129; Conservative
                                                                                                                                                                                      PILGRIM M.
ADAM L.
RIECHMANN J L.
                                                                                                                                                                                                                                                                                                                                             WPI; 2001-335977/35.
                                                                                                                                           JIANG C.
HEARD J.
                                                                                                                                                                                                                                                            SAMAHA R.
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                                                17-NOV-1999;
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;
                                                                                                                                                                                                                                                                                      Arabidopsis thaliana protein fragment SEQ ID NO: 24073.
                                                                                                                                                    AAG21497 standard; Protein; 272 AA
                                       286 -----ggggmgs 292
244 FOFSGGDIYGMSGGSGGGGGA 265
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99US-0128714.
99US-0129845.
99US-0130077.
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99US-0132484.
99US-0132485.
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99US-0134370.
99US-0134768.
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99US-0123548
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99US-0135629
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tive 37; Mismatches 58
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AL161547 Arabidops AL021635 Arabidops AL161558 Arabidops

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ATF23E12 86710 bp DNA linear PLN 01-APR-1999® Arabidopsis thaliana DNA chromosome 4, BAC clone F23E12 (ESSA
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Arabidopsis thaliana
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Rosidae; eurosidas II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 86710)
Bevan, M., Hilbert, H., Braun, M., Holzer, E., Brandt, A.,
Duesterhoeft, A., Hohelsel, J., Mewes, H.W., Mayer, K.F.X. and
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EU Arabidopsis sequencing, project.
Direct Submission
Submitted (01-APR-1999) MIPS, at the Max-Planck-Institut fuer
Biochemie, Am Klopferspitz 18a, D-82152 Martinsried, FRG, E-mail:
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AUTHORS
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10599.682 Million cell updates/sec
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                                                                                                                         July 10, 2002, 19:01:52; Search time 1922.93 Seconds
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            GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                          1797656 seqs, 10463268293 residues
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Maximum Match 100%
Listing first 45 summaries

    nucleic search, using sw model

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Database :

AP003938 Oryza sat AP004680 Oryza sat AP004303 Oryza sat AF429315 Homo sapl

AJ234403 Hordeum v AF474373 Hordeum v

AC012188 Sequence AF184830 Arabidops

166494 Sequence 14 AF429315 Homo sap1 AJ132349 Antirrhin AJ224119 Arabidops

AP004165 Oryza saf AL162281 Oryza sat AL132275 Arabidops AC011437 Arabidops AP001526 Oryza sat AP003891 Oryza sat AP004597 Oryza sat AP004635 Oryza sat

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/product="clathrin assembly protein AP19 homolog"
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/note="Contains Clathrin adaptor complexes small chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(join(4939, .5013,5109, .5195,5307, .5342, 5451, .5651,5725, .5811,6161, .6163))
4939, .6163
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Lahiwklegakerlrlvkadlmeegspdnaimgcogvfhtaspeilrpaiegtlnvlr
Scrknpslkrvvltsssstvwyalsktlaeqaawkfseengidlvtvlpsflvgpslp
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NRPKDIFVNDLCSRSGGKCKVPWTVTPDMDLLAAQTIMNKHELSHVAVVSGSIDAPRI
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                                                                                                                          Information on performance of analysis and a more detailed annotation of this entry and other sequences of chromosomes 3, 4 and 5 can be viewed at: http://www.mips.biochem.mpg.de/proj/thal/. Location/Qualifiers
      schuelle@mips.biochem.mpg.de,mayer@mips.biochem.mpg.de Project
Coordinator: Mike Bevan, Molecular Genetics Department, Cambridge
Laboratory, John Innes Centre, Colney Lane, NR4 7UJ Norwich, UK,
E-mail: michael.bevan@bbsrc.ac.uk
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                                                                                                                                                                                                                                                 1. .86710
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FEATURES

COMMENT

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Information on performance of analysis and a more detailed annotation of this entry and other sequences of chromosomes 3, 4 \,
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6GETNVVSESGGGEEGAQDAAKTTPEGEADRI"
8233. 9045
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                                                                                                                                                                                                                                                                                                     /note="similarity to DNA-binding protein PD1, Pisum
                                                                                                                                                                                                                                                                                                                                                                  Query Match 97.8%; Score 952.8; DB 8; Length 86710; Best Local Similarity 99.7%; Pred. No. 2.1e-258; Matches 965; Conservative 0; Mismatches 2; Indels 1;
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Arabidopsis thallana DNA chromosome 4, contig fragment No. 83.
AL161587
AL161587.2 GI:7270470
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Hilbert, H., Braun, M., Holzer, E., Brandt, A., Duesterhoeft, A., Mewes, H.W., Lemcke, K. and Mayer, K.F.X.
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Robben, J., Grymonprez, B., Volckaert, G., Mewes, H.W., Lemcke, K. and
Mayer, K.F.X.
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8500 GTTACCGATTGAAGAGAAGAAACCCCACCGCGGGAACCACCGGGTGCAGCAGCAGCAGA 8441
                                                                                                                                                                                                                                                                                                                              8440 GCCGGAGGCGTCTCAGTCGTCGGAGGTTACGGGGAGTGGGGCCCCAGGCGTGTGAGTCAAA 8381
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                                                                                                                                                                                                                        667 gccggaggcgtctcagtcgtcggaggttacggggagtggggccaggcgtgtgagtcaaa 726
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                                                                                                               607 gttaccgattgaaggaagaagccccaccgccgagaaccaccggggtgcagcagca
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Murphy,G., Ridley,P., Hudson,S., Mewes,H.W., Lemcke,K. and
Mayer,K.F.X.
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EU Arabidopsis sequencing, project.
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Location/Qualifiers
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CEGROSTER OF "MGCCOSLESGONPLGKDGVQPQPLSQNNHGGATTADNGGSGGAS OF VGGGGGGGGTBEFSEPESPEDLAATHNESDNIVSESGERAPNLYYKGRLONRRWIN VKKFTRMAMPERPORPEBLAMGVGKLHHNRLANLIGYCCDGDERLLVAEFMPNDTLAKH LEHWENQTIEHAMRLRVGYTIAEALDYCSTEGRELXHDINATRYLEDEGDPRLLSCKFIRKSRCFIRKSRCFIRKSTSTYLLDLLGSKHIPPSHALDD DVPSYVMLGIKKOEEAPSTPQRATVPESYYSTGTYLLDLLGSKHIPPSHALDD DVPSYVMLGIKKOEEAPSTPQRPLSFLGGAGSRMLATHOLDGAGSKHIPPSHALDD TOVPSYVMLGIKKOEEAPSTPQRPLSPLGEAGSRMLATHOLDGAGSKHIPPSDEGOTNELD TVFGRRENDLANDSHIPREDDEGOTNELD TVFGR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97.8%; Score 952.8; DB 8; Length 197859; 99.7%; Pred. No. 2.2e-258; 1.1ve 0; Mismatches 2; Indels 1;
                                                                                                                                                                                                                                                                                                             complement(19941, .20231)
/gene="AT4g35230"
/number=1
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/gene="AT4g35230"
/db_xref="GI:7270475"
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Best Local 3
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PLN 10-NOV-1999
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Weigel,D., Ahn,J.H., Blazquez,M.A., Borevitz,J., Christensen,S.K.,, Fankhauser,C., Ferrandiz,C., Kardallsky,I., Neff.,M.M., Nguyen,J.T., Sato,S., Wang,Z., Xia,Y., Dixon,R.A., Harrison,M.J., Lamb,C.J., Yanofsky,M.F. and Chory,J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      development; similar to F9H16.12 encoded by GenBank
Accession Number AC007369; similar to AT-hook proteins and
pea PDI homolog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="MEGGYEQGGGASRYFHNLFRPETHHQQLQPQGGTNLIDQHHHQH
QQHQQQQQPSDDSRESDHSNKDHHQQGRPDSDPNTSSSAPGKRPRGRPPGSKNRAKPP
IIVTROSPNALRSHVLEYSPGADIVESYSTYARRGRGVSVLGGNGTVSNVTLRQPVT
PGNGGGVSGGGGVVTLHGRFEILSLTGTVLPPPAPPGAGGLSIFLAGGQGQVVGGSVV
APLIASAPVILMAASFSNAVFRRLPIEEEEECGGGGGGGGPPQMQQAPSASPPSG
VTGQGQLGGNVGGYGFSGDPHLLGWGAGTPSRPPF"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="overexpression causes late flowering,modified leaf development; similar to F9H16.12 encoded by GenBank
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Institute for Biological Studies, 10010 N. Torrey Pines Road,
                                                                                                                                                                                                                                                                                                                                                                      Arly4974 13023 bp mRNA linear PLN
Arabidopsis thaliana ESCAROLA (ESC) mRNA, complete cds.
AF194974
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Unpublished
2 (bases I to 1323)
Muyen, J.T., Christensen, S.K. and Weigel, D.
Direct Submission
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/db_xref="GI:6319180"
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e-mail for correspondence: arabégequence.stanford.edu
cenes with similarity to proteins in the databases are described as
'putative', '-like' or 'similar to'. Genes that have EST
similarity but no significant protein similarity are described as
'unknown proteins'. Genes that are annotated based only on gene
prediction software are described as 'hypothetical proteins'.
The software programs used to predict genes include: Grail
(Informatics Group, Oak Ridge National Laboratory,
http://compbio.ornl.gov/section/index.html), GENSCAN (Chris Burge,
http://compbio.ornl.gov/section/index.html), Fexa (V.Solovyev)
ttp://ground.c.stanford.edu/-chris/GENSCANW.html), Fexa (V.Solovyev)
NetplantGene (S.M. Hebsgaard, et al., CBS, Technical University of
Denmark,htp://www.cbs.dtu.dk/NetPlantGene.html).
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NKKPRPRSVEFPASPQLVQGEEMVHFGHPQHYLVKYELPDIYTCAGCKEEGAGVRYVC
QECTOYQLHEFASFAPPQLKSHPFHYQHQHQLLFFPAFPAKGGIVXSKCDVGGRSPKGYTFR
CRCTSCMHPGCAMAPSPLLSSSLHHHPLRLLPSSSAGSTTGGDSGFLCGECKRGKR
TGRVYRCTVCDYHLHAVCAKDAAVNGLRANGHKGRDKSPAJLGTAARLASQVVIDFLG
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LNERROPRICKGYTNTCEICCRSLLDSFRFCSLGCKLGGMRRGDLSLTFSLKGKHGRE
YLGGSESDEATTPTKMRKTNAFNRLMSGLSISTVRFDDYGPNGDQRSSSSGDEGGFSF
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                                                                                                                                                                                                                                                                                                                                                                                       Federspiel.N.A., Palm.C.J., Conway, A.B., Conn, L., Hansen, N.F., Faderspiel.N.A., Palm.C.J., Conway, A.B., Conn, L., Hansen, N.F., Ataijo, R., Huizar, L., Rowley, D., Buehler, E., Dunn, P., Gonzalez, A., Kremenetskaia, I., Kim, C., Lenz, C., Li, J., Liu, S., Luros, S., Schwartz, J., Shinn, P., Toriumi, M., Vyotskaia, V., Walker, M., Yu, G., Ecker, J., Theologis, A. and Davis, R.W. Submitted (17-MAY-1999) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304,
                                                                                          Federspiel, M.A., Palm, C.J., Conway, A.B., Conn, L., Hansen, N.F., Altafi, H., Araujo, R., Huizar, L., Rowley, D., Buehler, E., Dunn, P., Gonzalez, A., Kremenetskaia, I., Kim, C., Lenz, C., Li, J., Liu, S., Luros, S., Schwartz, J., Shinn, P., Toriumi, M., Vyotskaia, V., Walker, M., Yu, G., Ecker, J., Theologis, A. and Davis, R.W. Direct Submission
                                                                                                                                                                                                                                                                                     Submitted (07-MAY-1999) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304,
Stanford University, 855 California Avenue, Palo Alto, CA 94304,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(join(8784. .9101,9359. .9574,9662. .9859))
/gene="F9H16.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    On May 7, 1999 this sequence version replaced gi:4678189.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GIIDGLGEGVGEAIIDGVTRGGGGGGGGGGGTRVIPRVRGG"
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γρατο="F9H16.2"
γρατο" -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Arabidopsis thaliana"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SPGTPPIYNHRNSSRRKGVPHRAPF"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /protein_id="AAD30592.1"
/db_xref="GI:4836889"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /protein_id="AAD30591.1"
/db_xref="GI:4836888"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(8784. .9859)
/gene="F9H16.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:3702"
/chromosome="1"
/map="m1203"
/clone="F9H16"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /cultivar="Columbia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="F9H16.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon_start=1
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1 (bases 1 to 103192)
Federspiel, N.A., Palm, C.J., Conway, A.B., Conn, L., Hansen, N.F., Altafi, H., Araujo, R., Huizar, L., Rowley, D., Buchler, E., Dunn, P., Gonzalez, A., Kremenetskala, I., Kim, C., Lenz, C., Li, J., Liu, S., Luros, S., Schwartz, J., Shinn, P., Toriumi, M., Vysotskala, V.S., Walker, M., Yu, G., Ecker, J., Theologis, A. and Davis, R.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Federspiel. N.A., Palm, C.J., Conway, A.B., Conn, L., Hansen, N.F., Altafi, H., Araujo, R., Huizar, L., Rowley, D., Buehler, E., Dunn, P., Gonzalez, A., Kremenetskaia, T., Kim, C., Lenz, C., Li, J., Liu, S., Luros, S., Schwartz, J., Shinn, P., Toriumi, M., Vyotskaia, V., Walker, M., Yu, G., Ecker, J., Theologis, A. and Davis, R.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -cggctggtggaggtgtgattaccctgcatggt 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             419 eggittigacaittigicittigaceggiacigesticeacegecigeaceaceggggagea 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         479 ggaggittgacggigiatctagccggaggicaaggacaagitgiaggagggaatgiggci 538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 929 GCTCCCCTTATTGCATCAGCTCCGGTTATACTAATGGCGGCTTCGTTCTCAAATGCGGTT 988
                                                                                                                                                                                                                                                                           140 gcctctggctcttcctccggacgtcgtccacgtggtcgtcctgcaggttccaaaaacaaa 199
                                                                                                                                                                                                                                                                                                                                        509 ACATCAAGCTCAGCACCGGGAAAACGTCCACGTGGACGTCCACCAGGATCTAAGAACAAA 568
                                                                                                                                                                                                                                                                                                                                                                                                    200 eccaaacctccgacgattataactagagatagtcctaacgtccttagatcacacgttctt 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gaagtcacctccggttcggacatatccgaggcagtctccacctacgccactcgtcgcggc 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 749 GTCACTCCTGGAAATGGCGGTGGTGTCCCGGAGGAGGAGGAGTTGTGACTTTACATGGA 808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             868
                                                                                                                                                80 gaagcagacgaagcaaaggccgagaccactcccaccggtggagccaccagctcagccaca 139
                                                                                                                                                                                                               449 GAATCTGACCATTCAAACAAAGATCATCATCAACAGGGTCGACCCGATTCAGACCCGAAT 508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (24-APR-1999) DNA Sequencing and Technology Center,
                                                                                          Gaps
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Arabidopsis thaliana chromosome I BAC F9H16 genomic sequence,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     539 ggttcgttaattgcttcgggaccggtagtgttgatggctgcttcttttgcaaacgcagtt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                629 GAAGTATCTCCTGGAGCTGACATAGTTGAGAGTGTTTCCACGTACGCTAGGAGGAGGAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               320 tgcggcgtttgcattataagcggcacgggtgcggtcactaacgtcacgatacggcaacct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                809 AGGITIGAGAIICITICGCIAACGGGGACIGITITGCCACCTCCTGCACCGCCTGGTGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       569 GCCAAGCCACCGATCATAGTAACTCGTGATAGCCCCCAACGCGCTTAGATCTCACGTTCTT
                                                                                          21;
                       Length 1323;
                                                                                          Indels
                          DB 8;
                                                                                          0; Mismatches 191;
                          Score 212.4; DB 8 Pred. No. 5.6e-49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     989 TTCGAGAGACTACCGATTGAGGAGGAGGAA 1018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       599 tatgataggttaccgattgaagaggaagaa 628
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                          21.8%;
62.8%;
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                                                                                                 Matches 358; Conservative
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Unpublished
                                                               Similarity
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AC007369/c
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COMPlement(join(18939. 19358,1941. 20040,20119. 20263, 20346. 20481,20575. 20246,22334. 22883,20975. 21049, 21141. 21943,22041. 22246,22334. 22883,20975. 21049, 21441. 21943,22041. 22246,22334. 228830,)
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//rotein_id="mbevgapper protein; location of ESTs; location of ESTs locat
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complement(27992. :33534)
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/note="Hypotchetical protein"
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WSVQTPLRQFHGLSNDILMQLEKKDLVWERYYDLSAQELGELTRSPKMGKPLHKFTHQ FPKVTLSAHVQPITRTVLNVELTVTPDFLWDEKIHKYVEPFWIIVEDNDGEKILHHEY

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                                                                                                        74674 GAATCTGACCATTCAAACAAAGATCATCATCAACAGGTCGACCCGATTCAGACCCGAAT 74615
                                                                                                                                                                                 74614 ACATCAAGCTCAGCACCGGGAAAACGTCCACGTGGACGTCCACCAGGATCTAAGAACAAA 74555
                                                                                                                                                                                                                                          74374 GTCACTCCTGGAAATGGCGGTGGTGTGTCCGGAGGAGGAGGAGTTGTGACTTTACATGGA 74315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 74254 GGTGGTTTGTCTATATTTTTAGCCGGAGGCAAGGTCAGGTGGTCGGAGGAAGCGTTGTG 74195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              260 gaagtcacctccggttcggacatatccgaggcagtctccacctacgccactcgtcgcggc 319
                                                                                                                                             140 gcctctggctcttcctccggacgtcgtccacgtggtcgtcctcgcaggttccaaaaacaaa 199
                                                                                                                                                                                                                                                                                                                                                                      320 tgcggcgtttgcattataagcggcacgggtgcggtcactaacgtcacggtacggcaacct 379
                                                                          gaagcagacgaagcaaaggccgagaccactcccaccggtggagccaccagctcagccaca 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ggttcgttaattgcttcgggaccggtagtgttgatggctgcttcttttgcaaacgcagtt 598
                                                                                                                                                                                                                                                                                                                                                                                                                                              ggaggtttgacggtgtatctagccggaggtcaaggacaagttgtaggagggaatgtgggct
                                                                                                                                                                                                                    200 cccaaacctccgacgattataactagagatagtcctaacgtccttagatcacacgttctt
                                                                                                                                                                                                                                                                                                                                                                                                       74434 AGAGGCGTCTCCGTTTTAGGAGGAAACGGCACCGTATCTAACGTCACTCTCCGTCAGCCA
   DB 8; Length 103192;
21.8%; Score 212.4; DB 8; Length 1
62.8%; Pred. No. 8.6e-49;
.1ve 0; Mismatches 191; Indels
               Best Local Similarity oz.o.
Matches 358; Conservative
 Query Match
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/note="Putative RNA helicase; Highly similar to human snRNP-specific 200kD protein, g113255965 and yeast

gene

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Arabidopsis thaliana chromosome II section 193 of 255 of the complete sequence. Sequence from clones T4C15, T3ZF12. AC004667 AE002093
HTG.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (09-MAR-2000) The Institute for Genomic Research, 9712 Medical Center Dr., Rockville, MD 20850, USA on Dec 17, 1999 this sequence version replaced gi:3668073. The sequence and annotation of chromosome 2 were merged from those of the individual clones on this chromosome after removing overlaps. For detailed information, please see the TIGR web site (http://www.tigr.org/tdb/at/at.html).
                                                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence and analysis of chromosome 2 of the plant Arabidopsis
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                                                                                                                                                                                                                                                             Arabidopsis thaliana
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                                                                                             DEFINITION
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              RESULT
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Genes were identified by a combination of three methods: Gene prediction programs including GRAIL (ftp://arthur.epm.orn.jcov/pub/xgrail), Genefinder (Phil Green, University of Washington), Genscan (Chris Burge, Durio.catalford.edu/GENSCARW.html), and NetplantGene (http://www.cbs.dtu.dk/services/NetGene2/), searches of the complete sequence against a peptide database and plant EST databases at TiGR, and manual curations based on those analyses. Annotated genes are named to indicate the level of evidence for their annotation. Genes with similarity to other proteins are named after the database hits Genes without significant peptide similarity but with EST similarity are named as 'unknown' protein or EST similarity are named as 'unknown' protein or EST similarity are named as 'unknown' protein or EST similarity are named as 'hypothetical' proteins. Genes without protein or EST similarity. That are predicted by two or more gene prediction programs over most of their length are annotated as 'hypothetical' proteins. Genes encoding tRNAs are predicted by tRNAscan-ES (Sean Eddy, here). http://genome.wustl.edu/eddy/tRNAscan-SE/). Simple repeats were identified by repeatmasker (Arian Smit, http://ftp.genome.washington.edu/RM/RepeatMasker.html). Genes are numbered from the top to bottom of the chromosome.

We thank the CSHL/WashU/ABI consortium for sequencing BAC clones F6P23, F5J6, T17A5, and T13L16, the ESSA group for sequencing clone F13D4, and Scott Jackson, Jiming Jiang, Klaus Meyer, Eric Richards and Satoshi Tabata for helpful assistance. In addition, we would like to thank the TIGR Bioinformatics Department, especially Lixin Shou, Hanif Khalak, Michael E. Heaney, Lily Fu, Feng Liang, Jeremy Peterson, Michael Holmes, and Delwood Richardson for software and database support.

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Address all correspondence to: at@tigr.org.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .8749,9119. .9154,9181. .9248,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    //note="T4C15.25; predicted by genscan"
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="At2g35080
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                            .88411
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       FEATURES
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COMMENT

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KEDDVTIKHGTQSRENRRAATKGMHTSKFCLNPAGDTPSACRLFDSIVSLCVPLIVSD
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LMSMHKPNRSYHFHLNNLFVFWERPFGLWRSLRRREFTETYTSRYSPLPWHNYFSGKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(join(15067. 15745,15828. 17044,17263. 17359, 17457. 17596,17686. 17811,18202. 18304,18567. 18712, 18931. 19124,1924,1923. 19531,19461. 19571,19810. 19942, 20057. 20031,20626. 20733,20868. 200993,21457. 21537, 21745. 21825,22206. 22280,22374. .>22775), complement(15067. >22775)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YSDEKMQEGLVEWLEGQEWWRRNAGRDHVIPAGDPNALYRILDRVKNAVLLVSDFGRL
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Arabidopsis thaliana chromosome II section 242 of 255 of the complete sequence. Sequence from clones T14P1, F4L23. AC002387, 2 GI:6598365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (09-MAR-2000) The Institute for Genomic Research, 9712 Medical Center Dr., Rockville, MD 20850, USA On Dec 17, 1999 this sequence version replaced gi:2583106. The sequence and annotation of chromosome 2 were merged from those of the individual clones on this chromosome after removing overlaps. For detailed information, please see the TIGR web site (http://www.tigr.org/tdb/at/at.html).
                     GTTGTGACTCTGCGGGGTACTTTTGAGATTCTTTCCCTCTCCGGATCTTTTCTTCCGCCA 76795
                                                                                                                                                                                  76796 CCTGCTCCTCCAGGGGGGGACTAGCTTGACGATATTCCTCGCTGGAGCTCAAGGACAGGTC 76855
                                                                                                                                                                                                                                                           76856 GICGGAGGTAACGIAGTIGGIGAGTTAATGGCGGCGGGGCCGGTAATGGTCATGGCAGCG 76915
                                                                                                                                                                                                                                                                                                                        cctgcaccaccgggagcaggaggtttgacggtgtatctagccggaggtcaaggacaagtt 520
   ggcacgggtgcggtcactaacgtcacgatacggcaacctgcggctccggctggtggaggt 400
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                                                                                                                                                                                                                                                                                                  tettttgcaaacgcagtttatgataggttaccgattgaagaggaagaaacccaaccgccg
                                                                          gtgattaccctgcatggtcggtttgacattttgtctttgaccggtactgcgcttccaccg
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KEYWORDS
SOURCE
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Genes were identified by a combination of three methods: Gene prediction programs including GRAIL (ftp://arthur.epm.orni.gov/pub/xgrail), Genefinder (Phil Green, University of Washington), Genscan (Chris Burge, http://gnomic.stanford.edu/GENSCANW.html), and NetplantGene (http://www.cbs.dtu.dk/services/NetGene2/), searches of the complete sequence against a peptide database and plant EST databases at TIGR, and manual curations based on those analyses. Annotated genes are named to indicate the level of evidence for

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F13D4, and Scott Jackson, Jiming Jiang, Klaus Meyer, Eric Richards and Satoshi Tabata for helpful assistance. In addition, we would like to thank the TIGR Bioinformatics Department, especially Lixin Zhou, Hanif Khalak, Michael E. Heaney, Lily Fu, Feng Liang, Jeremy Peterson, Michael Holmes, and Delwood Richardson for software and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="WNKGSIFKMDDDFEKRKAEAGRIREKYDDRIPVIVEKAEKSEVP
NIDKKKYLVPSDLTVGQFVYVIRKRIKLSAEKAIFIFVDNVLPPTGELMSSVYEDKKD
EDGFLYITYSGENTFGASSI"
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/db_xref="GI:2583134"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APAVKPTCPTDTLKLGVCADLLGLVNVVVGSPPKTPCCTLLQGLANLEAAVCLCTALK
                       after the database hits. Genes without significant peptide similarity but with EST similarity, that are named as 'unknown' proteins. Genes without protein or EST similarity, that are predicted by two or more gene prediction programs over most of their length are annotated as 'hypothetical' proteins. Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy. http://genome.wustl.edu/eddy/tRNAscan-SE). Simple repeats were identified by repeatmasker (Arian Smit,
their annotation. Genes with similarity to other proteins are named
                                                                                                                                                                                                                                                        http://ftp.genome.washington.edu/RM/RepeatMasker.html). Genes are
                                                                                                                                                                                                                                                                                                                                       We thank the CSHL/WashU/ABI consortium for sequencing BAC clones
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(join(<6393 .6470,6586 .6663,7082 .7157,7248 .7296,7872 .8004,8099 .8260,8382 .>8495))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /monthement(519. .627)
/rpt_family="(TAAAA)n"
join(2227. .2322,2480. .2527,2650. .2705,3098. .3150,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               join(2488. .2527,2650. .2705,3098. .3150,3250. .3469)
/gene="At2g45170"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This work was supported by the National Science Foundation, Department of Energy and the US Department of Agriculture.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="putative microtubule-associated protein"
                                                                                                                                                                                                                                                                                  numbered from the top to bottom of the chromosome.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Address all correspondence to: at@tigr.org.
Location/Qualifiers
1. .122871
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(<1. .2952)
/note="Sequence from clone T14P1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Sequence from clone F4L23"
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/gene="At2g45180"
4282. .4870
/gene="At2g45180"
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/gene="At2g45170"
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/gene="At2g45170"
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4320. .4724
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3250. .364
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YDLTYSKINETMIDPNYKCSKLDAQTMLSTALTNILDTCRAGFIELGVTDIVUPLMSNNV
SNLLCNTLAINKVPFNYTPPEKDGFPSWVKPCDRKLLQSSTPKDNAVVAKDGSGNFKT
SKADIDAASGSGRFVIYVRQYYSENDEJRKKNVMLRGDGIGKTIITGSKSVGGTTT
FNSATVAAVGDGFIERGITFENTAGASUBQNYALRSGSDLSYFYQCSFEAYQDTLYVH
SNRQFYRDCDVYGTVDFIFGNAAAVLONCNIFARRPFRSKTNTITAQGRSDPNONTGII
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Dilhbytoefrrikgininslrehaellssyrddisbyksgswspsygvylrefalsind
Sishiddvidgoatravigsorslesdvogkvknigdkfpvirgilgsirkrrsrdt
Lilsavitaactlelitwisk"
complement(17986. 18862)
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/db_xref="E1:20883132"
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FLTHNSNNEPIKSESEFLKISMKLVLDRAILAKTHAFTLGPKCRDTREKAAWEDCIKL
                                                                                                                                                                                                                                      SLEKTYTYRCGCCTNILLSVNRRSYYLPASNOLOLOLGPHSYFNPODILEELRDAPSNM
NAMMANQHPTMNDIPSFMDLHQQHEIPKAPPVNRPPEKRQRVPSAYNRFIKEEIQRIK
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/2613. .12646

/rpt_family="(CATA)n"

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16252. .1634,1.16810. .17006,17451. .17647))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(join(15632. 15729,15821. 15950,16066. 16137,
16252. 16341,16810. 17006,17451. 17583))
/gene="At2g45200"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="F4L23.28; member of auxin-induced protein multigene
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VYFNHPLFGELLREAEKEYGFCHEGGITIPCLYSDFERVKTRIASGSSSRVFPWGRHC
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/db_xref="G1:2583133"
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/protein_id="AAB82640.1"
/db_xref="G1:2583131"
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|/gene="At2g45210"
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/gene="At2g45200"
                                                                                                                                                        /protein_id="AABB2644.1"
/db_xref="G1:2583135"
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Genes were identified by a combination of several methods: Gene prediction programs including Genscan+ (Chris Burge, http://CCR-081.mit.edu/GENSCAN.html), GeneMarkHMM (Mark Borodovsky, http://GCR-081.mit.edu/GENSCAN.html), GeneMarkHMM (Mark Borodovsky, http://genemark.blology.gatech.edu/GeneMark/), GilmmerA (a varlant of GlimmerM, see Mihaela Pertea, http://www.tigr.org/softlab/gilmmerm_htm/gilmmerm.html, and GeneSplicer (Mihaela Pertea and Steven Salzberg, contact mpertea@tigr.org), searches of the complete sequence against a peptide database and the plant EST database at TiGR (http://www.tigr.org/tdb/tgi.shtml). Annotated genes are named to indicate the level of evidence for their annotation. Genes with similarity to other proteins are named after the database hits. Genes without significant peptide similarity but with EST similarity, that are predicted by more than two gene prediction programs over most of their length are annotated as hypothetical proteins. Genes encoding tRNAs are predicted by tRNAscan SE (Sean Eddy, http://genome.wuslington edu/RW/Repeatmasker (Arian Smit, http://ftp.genome.washington edu/RW/Repeatmasker html).
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LIAVSRCAWLRRIASRNRSDQTHPPPVAAANKGLKKKVLRSLPKLTYSPDSPPAEKLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ECAICLTEFAAGDELRVLPQCGHGFHVSCIDTWLGSHSSCPSCRQILVVTRCHKCGGI
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/gene="F14G6.2"
                                 2 (bases 1 to 100806)
Lin,X. and Kaul,S.
Lin,X. and Kaul,S.
Lin,X. and Kaul,S.
Submitted (16-NOV-1999) The Institute for Genomic Research, 9712
Medical Center Dr. Rockville, MD 20850, USA, xlin@tigr.org
Town,C.D. and Kaul,S.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="contains Pfam profile: PF00097 Zinc finger, C3HC4
                                                                                                                                                                                                                                                                                                                                                                                                                   BAC clone F14G6 is from Arabidopsis thaliana chromosome 1
The orientation of the sequence is from SP6 to T7 end of the BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="35000 nt before this point were not included in the submitted sequence, due to overlap with another BAC
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/protein_id="AAG51946.1"
/db_xrefe="GI:12323975"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Complement(8331. .10137)
/gene="F1466.2"
/note="N-term similar to N-term of NAM GB:CAA63101
[Petunia x hybrida] (apical meristem formation), CUC2
GB:BAA19529 [Arabidopsis thaliana], GRAB2 protein
GB:CAA09372 [Triticum sp.]"
complement(join(8331. .8855,9526. .9800,9933. .10137))
                                                                                                                                                                                                                                                                    Submitted (19-JAN-2001) The Institute for Genomic Research, 9 Medical Center Dr. Rockville, MD 20850, USA, cdtown@tigr.org On Jan 19, 2001 this sequence version replaced g1:12280761. Address all correspondence to:at@tigr.org
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/chromosome="1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 <5217. .>5774
/gene="F14G6.1"
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/gene="F14G6.1"
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/gene="F14G6.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="F14G6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         [F15M4]"
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TITLE
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                 COMMENT
IHNSRVTAASDLRPVLGSTKTYLGRPWRQYSRTVFMKTSLDSLIDPRGWLEWDGNFAL
KTLFYAEFONTGPGASTSGRVTWPGFRVLGSASEASKFTVGTFLAGGSWIPSSVPFTS
                                                                                                                                                                                                                                                                                                                                                         1;
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1 (bases 1 to 108060; Brito, M.-I., Creasy, T.H., Haas, B.J., M.D., Malti,R., Rouning,C.M., Moo,H., Pulli,L.C., Otterback,T.R., Barnstead,M.E., Bowman,C.L., White,O., Nierman,W.C. and Fraser,C.M. Arabidopsis thaliana chromosome 1 BAC F14G6 genomic sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PLN 15-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                         Db 105952 TGATATCGATCCCAACGACCACTTTCAGCCGGAAAAGATCAAAGTACTCCTGGCTCCGG 106011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DD 106072 ACCAGGGGATCTAAGAACAAAACGCGCAATCATCATCACTCGAGACAGCGGGAAA 106131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Db 106132 CGCTCTCAAATCTCATGTCATGGAAGTAGCAAACGGATGTGACGTCATGGAAAGTGTCAC 106191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Db 106012 TGGAGAAAGCGGCGGCGGGGGGGGGGGGTAATCACATCACGAGAAGGCCACGTGGCAG 106071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   D 106372 AGCTGCGTCAGGTCTAAGGATTTACTTAGCCGGTGGTCAGGGACAGGTTGTTGGAGGAAG 106431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DD 106432 CGTGGTTGGTCCACTCATGGCTTCAGGACCTGTAGTGATTATGGCAGCTTCGGAAA 106491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DD 106192 CGTCTTCGCTCGCCGTCGCCAACGTGGCATCTGCGTTTTGAGCGGAAACGGCGCCGTTAC 106251
                                                                                                                                                                                                                                                                                                                                                                                                       58 taacatggaacttaacagatctgaagcagacgaagcaaaggccgagaccactcccaccgg 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     118 tggagccaccagctcagccacagcctctggctcttcctccggacgtcgtccacgtggtcg 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           238 cgtccttagatcacacgttcttgaagtcacctccggttcggacatatccgaggcagtctc 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            298 cacctacgccactcgtcgcggctgcggcgtttgcattataagcggcacgggtgcggtcac 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             358 taacgtcacgatacggcaacctgcggctccggctggtggagg----tgtgattaccct 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 532 tgtggctggttcgttaattgcttcgggaccggtagtgttgatggctgcttcttttgcaaa 591
                                                                                                                                                                                                                                                                                                                                                      6; Gaps
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Arabidopsis thaliana chromosome 1 BAC F14G6 genomic sequence,
complete sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             178 tcctgcaggttccaaaaacaaacccaaacctccgacgattataactagagatagtcctaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               412 gcatggtcggtttgacattttgtctttgaccggtactgcgcttccaccgcctgcaccacc
                                                                                                                                                                                                                                                                                            DB 8; Length 122871;
                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                        Pred. No. 9.5e-47;
0; Mismatches 218;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Db 106492 CGCTGCCTATGAGACTGCCGTTGGAGGAAGACGA 106527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     592 cgcagtttatgataggttaccgattgaagaggaaga 627
                                                                               23009. .23038
/rpt_family="(TA)n"
28701. .28741
/rpt_family="POLY_A"
complement(29132. .29228)
/rpt_family="POLY_A"
                                                                                                                                                                                                                                                                                            Score 205.2;
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61.1%;
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                                                                                                                                                                                                                                                                                                                                             Matches 352; Conservative
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AC015450
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DEFINITION
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AUTHORS
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KEYWORDS
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complement(join(<26257. .26401,26478. .26667,26773. .26935,
27062. .27247,27332. .27486,27593. .>27736))
/gene="F14G6.7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="MAYROKVCYTGAGGFIASWLVKFLLSRCYTVHGTVRDPCDEKND HLRKLDNASKNLKLFKADLFDDEGLFSAIDGCSGVFHIASPVPFEGFELIKFALTGTK NVLRGACTETKVOKVVVVSIAAVVTNPRWPQDYSKDEGCWSDTQYLHSLERYTYTAKT LTEREALEWSKRNFADVVTLCPSVIIGPFKASSLGLIKFIKGGIKSLLSDELY LVDVRDVADALLLYSRREATGRYICKSHLSTDSLAGKKKNMYPKRNFPESFTEVKE KEVRFLSAEKLKNLGWFFRPFEETIDDSVVSFAGGILKA
                                                                                                                                                                                                                                                                                                                               GPEYMYSQSQCLYSPYMGQQYLQVYGVPGAVNSPVYQYGQLSQTIPNGHGYTAVQGYS
VPGSHILQLGGPTVSTMTTSSMPALQAPYPSGIPGPAPVQSHIIVHSPQFMQSTASDQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(join(<28495. .28664,28744. .28834,28902. .29033,
                                                                                                                                                                                                                                                                           EQYGELLEAVVIADKNTGRSKGYGFVTFRDPEAARRACADPTPIIDGRRANCNLASLG
RPRPPLPYAVIPNMPDLLPRTLEMCRVLEVHLLEIIRISNHFHITTSKELSILMVTAY
                                                                                                                                                                                                                                              /translation="MAYQPVPGSGFHYLNSPFGDTTFTKVFVGGLAWETQSETLRQHF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(join(26257. .26401,26478. .26667,26773. .26935,
27062. .27247,27332. .27486,27593. .27707))
/gene="F14G6.7"
                    motif. (a.k.a. RRM, RBD, or RNP domain)"
complement(join(23340, .23431,23548, .23785,23879, .23919,
24008, .24124,24234, .24378,24602, .24808))
/gene="F14G6.6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="putative cinnamoyl-CoA reductase; 27707-26257" /protein_id="AAG51951.1" /db_xref="GI:12323980"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="similar to cinnamoyl-CoA reductase GB:CAA56103 [Eucalyptus gunnii]; contains non-consensus GG acceptor splice site at exon 4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         42075 CCAAGAACAAGCCGAAGCCACCGGTGATAGTGACTAGAGATAGCCCCAACGTGCTTAGAT 42134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     42195 GCAGGAGGAGGAGGAGTCTCCATTCTCAGTGGTAACGGCACGGTGGCTAACGTCAGTC 42254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             42315 CICIACAIGGAAGGIIIGAGAIACIIICCCICACAGGIACGGIGIIGCCGCCCCCCTGCGC 42374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tacggcaacctgcgggctccggctggt------ggaggtgtgatta 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ccctgcatggtcggtttgacattttgtctttgaccggtactgcgcttccaccgcctgcac 467
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="contains Pfam profile: PF00076 RNA recognition
                                                                                                                                                                 /product="putative RNA-binding protein; 24808-23340"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                189 ccaaaaacaaacccaaactccgacgattataactagagatagtcctaacgtccttagat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cacacqttcttgaagtcacctccggttcggacatatccgaggcagtctccacctacgcca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ctcgtcgcggctgcggcgtttgcattataagcggcacgggtgcggtcactaacgtcacga
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="contains nonconsensus splice site"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches 167;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(26257. .27736)
/gene="F14G6.7"
                                                                                                                                                                                             /protein_id="AAG51948.1"
/db_xref="GI:12323977"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              qq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ΟŊ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AYIERVSLPGIEKNOOKIKEETOREGROVIQGVIPEIAIPSDIGGLYRMQVQQLCPPG
PFSITENLFQQVDPRLFSPNRRSDGIFEVVVVKLGVRIPTS"
Join(~20920. .20986,21073. .21148,21227. .21330,21407. .21472,
21739. .21821,21911. .21986,22064. .22182,22264. .22308,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          join(20920. .20986,21073. .21148,21227. .21330,21407. .21472,
21739. .21821,21911. .21986,22064. .22182,22264. .22308,
22385. .22411)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24008. .24124,24234. .24378,24602. .>24808))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KMISOIYYHKOSIGTALLSTSYAIALLGTALGQLIFGYLGDRVGRRKVYGLSLLIMVF
SSFCGFSVCTTRRSCVMVSLGFFRPVLGIGIGGDYPLSATIMSEFARKRTRGAFIAA
VFRMGLGLILIMSSAVTMVVCLAFKNBGESSEKTNVBGLETLAPPESDIAMRLILMIG
ALPALTFYWRMLMFTARTALTALVENNVVQAAKDMORVMSVSHISOITEDSSSELEQP
PSSSSSYKLFSRRFLSLHGRDLFAASANWFLVDVVFYTSNLLLSQIFNFSNKPLNSTNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YDSAFEVAKLAAIVAACSTIPGYWFTVYFIDKIGRVKIQMMGFFLMAVVYLVAGIPYS
WYWSKHEKTINKGFMVLYGLIFFFSNFGPNTTTFIIPAELFPARFRSTCHGISGAAGKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GAIVGTVGFLWATRHHEEDGFPDVKRVRIAFLILGGVCIAGMIVTYLFTRETMGRSLE
ENEDEIVSTSAGSSPANELLRRQY"
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HRISSRDHVGMKRRDVMLQIASSVFFLPLAISPAFAETNASEAFRVTDETNKFEISI
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                                                                                                                                                                                                                                                          PSLLYDDPHQNYNNNNFLHGSSGHNIDELKALINPVVSQLNGIIFPSGNNNNDEDDFD
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                                                                                                                                                                                                   WKATGKDKEVFSGGGGQLVGMKKTLVFYKGRAPRGLKTKWVMHEYRLENDHSHRHTCK
                                                                                                                                                                                                                                                                                    FNLGVKTEQSSNGNEIDVRDYLENPLFQEASYGLLGFSSSPGPLHMLLDSPCPLGFQL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /qene="F14G6.5"
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complement(join(8658. .8727,8813. .8910,9144. .9254,
9361. .9412,9514. .9665,9717. .9773,9878. .9978,10067. .10163,
10251. .10363.10862. .11027))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(join(8658. .8727,8813. .8910,9144. .9254,
9361. .9412,9514. .9665,9717. .9773,9878. .9978,10067. .10163,
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DGSEIVCEGPRCSLRSKKNITLDSLFGTNSRDVIDLMTSLIMQVYSDLAIDYFKMFLL
NVFATVVALGLFFFLDDITGFEITYLLELPEPFSFIFTWFAAVPAIVYLALSLTKLIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KDFLILKGPCPNCGTENVSFFGTILSIPNDSNTNNVKCSGCGTEMVYDSGSRLITLPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LLPLKASTDQSGQVGGEEVDSKILPYCSINKNEKRTIGEMEQEFLQAMQSFYYEGKAI
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complement(8658. .8727)
/gene="F16J13.30"
                                                                                                                                                                                                       complement(6594. .7577)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="F16J13.30"
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/number=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(9514. .9665)
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                                                                                                                                                                                                                                                                                                                                                                              /number=1
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                                                                                                                                                                                                                                                         /number=]
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                                                                                                                                                                                                                 AFF16J13 107600 bp DNA linear PLN 14-APR-1999
Arabidopsis thaliana DNA chromosome 4, BAC clone F16J13 (ESSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EU Arabidopsis sequencing, project.

EU Arabidopsis sequencing, project.

Burect Submission

Submitted (14-APR-1999) MIPS, at the Max-Planck-Institut fuer

Submitted (14-APR-1999) MIPS, at the Max-Planck-Institut fuer

Schuelle@mips.blochem.mpg.de,mayer@mips.blochem.mpg.de Project

Coordinator: Mike Bevan, Molecular Genetics Department, Cambridge
Laboratory, John Innes Centre, Colney Lane, NR4 7UJ Norwich, UK,

E-mail: michael.bevan@bbsrc.ac.uk

Information on performance of analysis and a more detailed

annotation of this entry and other sequences of chromosomes 3, 4

and 5 can be viewed at: http://www.mips.blochem.mpg.de/proj/thal/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="putative protein"
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GNISNPFPFRQEASEKFFFAWSLLSNPTIKEMYDYAFSDEVNLEPOGNVNEYMDYDS
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                                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis thallana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brasslcaceae; Arabidopsis.
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Arabidopsis thaliana"
42435 GAAACGIGGIGGCICCGCTIGIGGCITCGGGICCAGIGAIACIAAIGGCIGCAICGIICI 42494
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 10760)
Bevan, M., Hilbert, H., Braun, M., Holzer, E., Brandt, A.,
Duesterhoeft, A., Bancroft, I., Mewes, H.W., Mayer, K.F.X. and
                                                                        Db 42495 CTAATGCAACTTTCGAAAGGCTTCCCTTGAAGATGAAGGA 42535
                                               588 caaacgcagtttatgataggttaccgattgaagaagaa 628
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/note="24bp A tandem repeat"
complement(6594. .7577)
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5417. .6920
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SSRDDYSTRSRABEPSSSGODEYNNILWHTPMSYPPTYVPNQDDLSRFHLAQQRG
YGVSPPELHTSPGGASNRFTEQDKSLRFNSWCLPLESPLANSLTDDDFLEMSYEETVET
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                                                                                                                                                                                                                                                                                                                                                                                                                                           similarity to RNA splicing-related protein - Rattus norvegicus, PID:41024790 contains EST gb:H37320, Aa651292" /codon_start=1
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15593. .15914,16264. .16324,16543. .16583)
/gene="F16J13.40"
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                                                                                                                                                       .10363)
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/number=7
                                                        .10163)
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                                                       complement(10067.
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/gene="F16J13.30"
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/gene="F16J13.30"
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64.6%;
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11789. .118
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The debases 1 to 190026)

Solution of this frame of the max-planck-Institut fuer

Direct Submission

Direct Submission

Submitted (10-MAR-2000) MIPS, at the Max-Planck-Institut fuer

Biochemie, Am Klopferspitz 18a, D-82152 Martinsried, FRG, E-mail:

Lemckedmips Jacohem. mpg.de, Mayeremips. Diochem.mpg.de Project

Coordinator: Mike Bevan, Molecular Genetics Department, Cambridge

Laboratory, John Innes Centre, Colney Lane, NR4 7UJ Norwich, UK,

E-mail: michael: Devandebbsrc.ac.uk

Information on performance of analysis and a more detailed

annotation of this entry and other sequences of chromosomes 3, 4

and 5 can be viewed at: http://www.mips.biochem.mpg.de/Proj/thal/

this fragment has an overlap with ATCHRIV32 at the 5' end and an

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATCHRIV33 190026 bp DNA linear PLN 16-MAR-2000 Arabidopsis thaliana DNA chromosome 4, contig fragment No. 33. ALI615133
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1 (bases 2832 to 3389; 3666 to 4213)
Volckaert, G., Grymonprez, B., Voet, M., Robben, J., Mewes, H.W., Lemcke, K. and Mayer, K.F.X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 (bases 123056 to 190026)
Peters,S.A., van Staveren,M., Dirkse,W., Stiekema,W., Mewes,H.W.,
Lemcke,K. and Mayer,K.F.X.
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catatecgaggeagtetecacetaegecactegtegeggetgeggegtttgeattataag 339
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Hilbert,H., Braun,M., Holzer,E., Brandt,A., Duesterhoeft,A.,
Whowes,H.W., Lemcke,K. and Mayer,K.F.X.
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13583. 13711
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VRDJKARNILLDSDLKRKIVGFELARTWQGENAAETTEIVGTVGYLDPEYTRSGRVS
VRSDYARGVILLISRRKAMSVDGDSLIKYVRRCWNRGEAIDVIHEVMREEERRYS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contains Prokaryotic membrane lipoprotein lipid attachment
site AA472-482; Protein kinases signatures and profile
                                                                                                                                                                                      Contains Protein Kinases signatures and profile AA44-66, Protein Kinases signatures and profile AA159-171"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="KI domain interacting kinase 1-like protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(join(7389. 7679,7778. 7928,8208. .8445,
8555. .8765,8889. .9043,9121. .9255,9322. .10690))
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complement(7389. .7679)
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5676. 5762
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.14406,14643. .14879, LSKKSSQGLTEFKNEVVLIIKLOHKNLVRLLGYCVEGDEKLLIYEYMSNKSLDGLLFD SEKSRELDMETRMKIVNGTTRGLQYLHEYSRLRIHRDLKASANILLDBINDKTSDFG TARTFGCKQTDDSTGTRTGTQYTHSPERYANGSPERANILLEIBISKKATR FVHNDQKHSLLAYEWESWCETKGVSIIDEPMCCSYSLEEAMRCIHIALLCVQDHPKDR ARLEGPATFEASKLKVLFLGVDEKKHPAKLPRTTTTHSDITAKLTLAISQSINNSQL QGWARKLFEDEVGEWKRVKCKMSLHYHCHISGGHFFLMLIAKLRYTTFCKELPYVLE PRAGDEYLLNNHPELQESPWYYFHNIPEYNKVECWGPLWBAMSQHQHDGRTHKKS ETLPELPCPDECKCCPTVARLEGQAIFEASKLNVKFLGVDEKKHPPNLDRTTFTHS DITAKLTLAISHSINNSQLQGWANRLYRDEVVAEWRKVKSNMSLHYHCHISGDHFLLD /translation="MCSLATNLLLPSKMKPVFPEKLSTSSLCVTTRRSKMKNRSIVPV PMISQIVYMLSNDNTLPIPKQPTFSNVLNGDQQLDYVFSINEATQTELEAR" complement(7680. .7777) /gene="AT4g11900" /note-"similarity to hypothetical protein F7H19.100
-Arabidopsis thaliana, PID:e1310060
Contains Zinc finger, C2H2 type, domain AA420-440
contains EST gb:z34017, 234018" join(13583. 13711,13978. 14151,14239. 1. 15546. 15719,15829. 15996,16238. 16588) /gene="AT4911910"

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LIAELRYFIFCKELPMVLKAFVHGDENMLNNYPELHEAFVWVYFHSNIPKFNKVECWG
               RLCEATSHDGCKTPTCEILPEPPCFDKCSCCFPTVSTIPWSHSHGCSHGEEDNNVAIA
GGNLLTKYMYKRSKRK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Biochemie, Am Klopferspitz 18a, D-82152 Martinsried, FRG, E-mail: Hencke@migbs.biochem.mpg.de,mayer@mips.blochem.mpg.de project Coordinator: Mike Bevan, Molecular Genetics Department, Cambridge Laboratory, John Innes Centre, Colney Lane, NR4 7UJ Norwich, UK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E-mail: michael.bevan@bbsrc.ac.uk information on performance of analysis and a more detailed annotation of this entry and other sequences of chromosomes 3, 4 and 5 can be viewed at: http://www.mips.biochem.mpg.de/proj/thal/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     77599 CGITGGAGGTAGTGGTGGGACCTITGTTGTTGTTGTGTCGGGTCCTGTGGTGGTTATGGCGGC 77540
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    77836 CATAGTTGACTGTATGGCTACGTTCGCTAGACGCCGCCAAAGAGGCGTTTGCGTTATGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           77776 CGGTACAGGAAGCGTTACTAACGTCACTATACGTCAGCCTGGATCGCCACC---TGGCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             580 ttcttttgcaaacgcagtttatgataggttaccgattgaagaggaagaaaccccaccgcc
                                                                                                                                                                                                                                                                                                                                                                                                                                       aactagagatagtoctaacgtcottagatcacacgttcttgaagtcacctccggttcgga
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gcctgcaccaccgggagcaggagtttgacggtgtatctagccggaggtcaaggacaagt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   77659 GCCTGCGCCGCCTGCAGCCACCGGACTAAGCGTTTACCTAGCCGGAGGACAAGGGCAGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tgtaggagggaatgtggctggttcgttaattgcttcgggaccggtagtgttgatggctgc
                                                                                                                                                                                                                                                        Length 190026;
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                                                                                                                                                                                                                                                                                                     0; Mismatches 167;
                                                                                                                                                                                                                                                          Score 196.8; DB 8
Pred. No. 2.4e-44;
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EU Arabidopsis sequencing, project.
Direct Submission
                                                                                                      /number=1
13978. .14151
/gene="AT4911910"
                                                                                                                                                                                          14152. .14238
/gene="AT4g11910"
                                                           13712. .13977
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14152. .14
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Best Local Similarity
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TITLE
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KEYWORDS
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/translation="MELASFIGRALEYSVFLLSAWQEFNDFGEDGGRSAKSLKPKFNA
FVNHVTTHTGQQLPVDMKILVAAAIALKGIGGLLFVFGSSLGAYLLLLHQAVATPIL
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complement(join(5668.5772,5865.5963,6051.6140,
fgene="AT4914420"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GSILITTANCKFFSNGFDLAWAQTAGSKTGAANKLHOWYESFKFVVAALLDLPWFTIA
ALNGHAAAAGLILALSHDYVFWRKDRCVLYMSEVDIGLSMPDYFSALVRAKIGTSAAR
RELLLSGKKIRGEEAVGLGIVDSAAYDSEEGVVVASVRLGEKLAAKKWSGEVYASIRK
SLYPELCGILGLETRVFATPKL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="MCTLEKRGDLFLLTLTGDGEHRFHPDTIATILSLLEQAKSQSTR
                                                                                                                                                                                                                                                                    complement(join(5668. .5772,5865. .5963,6051. .6140,6238. .6352,7168. .7235))
//gene="AT4g14420"
//note="strong similarity to Nicotiana tabacum ORF able to induce HR-likelesions, PATX:G1762945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="similarity to carnitine racemase, Escherichia coli
contains EST gb:H36845, A1992737.1, T76583"
      an
    end and
this fragment has an overlap with ATCHRIV38 at the 5' overlap with ATCHRIV40 at the 3' end.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="carnitine racemase like protein"
/protein_id="CAB78485.1"
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LLGSGKKLKGEBAVALGIVDSAAHDSAEGVVEATVSLGESLAAKKNNGEVYATIRKSL
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ASRTSLFDGLDGLEEGRLRASSSYAHDERDNDEALENLQDRVSFLKRVCFFHLYN"
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TWLMNSVDKKIGGSLLYIATVQGIWNNLLSRPKQDDAPRIFDIEGKLSKIEGGSMDIS
TYYTALLTLWEEHRNYVELPVCTCGRCECDAAVKWEHLQQRSRVTKFLKELNEGFDQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="similarity to simlarity to retrovirus-related polyprotein (retrotransposon Tal-3), Arabidopsis thaliana" /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="retrovirus-related like polyprotein"
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TVRPNQKPICTHCGKVGHTIQKCYKVHGYPPGMKTGNTGYTYKPNPQLHVQPRMPMMP
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NLSLQDFTPQQIEQMISQFQAQVQVPEPAASSSNPSPLATVSEHGFMALTSTSGTIIP
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VHITQKLILHNVLHVPDFKFNLMSVSSLVKTISCSAHFYVDCCLIQELSQGLMIGRGR
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ILNVARALLFQSNIPMQYWSDCVTTAVFLINRLPSPLLNNKSPYELILNKQPDYSLLK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="similarity to adenylate cyclase (EC 4.6.1.1) II,
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AQGFTQQEGIDFLDTFSPVAKLTSAKMMLGLAAITGWTLTQMDVSDAFLHGDLDEEIF
MSLPQGYTPPAGTILPPNPVCRLLKSIYGLKQASRQWYKRFVAALVYIDDIMIASNND
AEVENLKALLRSEFKIKDLGPARFFLGLLGCKPSSIPMDPTLHLVRDMGTPLPNPTAY
                                                                                                                                                                                  RKLIGRLLYLTTRPDITYAVHQLSQFISAPSDIHLQAAHKVLRYIKANPGQGLMYSA
DYEICLNGFSDADWAACKDTRRSISGFCIYLGTSLISWKSKKQAVASRSSTESEYRSM
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                                                                            KSEKWIRVAVEELQAMELNKTWSVESLPPDKNVVGCKWVFTIKYNPDGTVERYKARLV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24787 GTCGCCGACACAATCGCTCACTTCTCAAGACGCAGGCAACGCGGCGTTTGCGTTCTCAGC 24846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24847 GGGACAGGCTCAGTCGCTAACGTCACCTCCGCCAAGCCGCCGCACC-----AGGAGGT 24900
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DQIKAGNLKALHVPTENQHADILTKALHPGPFHHLLRQMSLSSLFLPNKPVRS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        401 gtgattaccctgcatggtcggtttgacattttgtctttgaccggtactgcgcttccaccg 460
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24901 GIGGICTCTCTCCAAGGCAGGTITGAAATCTTATCTTTAACCGGIGCTTTCCTCCCTGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19.7%; Score 191.6; DB 8; Length 197976; 64.7%; Pred. No. 7.1e-43;
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/gene="dl3200c"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="strong similarity to ribosomal protein L41, Candida
                                                                                                                                                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (25-UNN-1999) MIPS, at the Max-Planck-Institut fuer Biochemie, Am Klopferspitz 18a, D-82152 Martinsried, FRG, E-mail: Biochemie, Am Klopferspitz 18a, D-82152 Martinsried, FRG, E-mail: Schuelledmips.blochem.mpg.de Project Coordinator: Mike Bevan, Molecular Genetics Department, Cambridge Laboratory, John Innes Centre, Colney Lane, NR4 7UJ Norwich, UK, Information on performance of analysis and a more detailed annotation of this entry and other sequences of chromosomes 3, 4 and 5 can be viewed at: http://www.mips.blochem.mpg.de/proj/thal/this fragment has an overlap with ATFCAO at the 5' end and an overlap with ATFCAO at the 3' end.
                                                                                                                                                                                                          Spermatophyta: Magnoliophyta; endicotyledons; core endicots; Rosidae; eurosidas II; Brassicales; Brassicaceae; Arabidopsis. 1 (bases 1 to 206606).

Bevan, M., Stiekema, W., Murphy, G., Wambutt, R., Pohl, T., Terryn, N., Freis, M., Kavanagh, T., Entlan, K.D., Rieger, M., James, R., Jones, J., Palme, K., Ansorge, W., Delseny, M., Bancroft, I., Mewes, H.W., Schueller, C. and Chalwatzis, N., Bancroft, I., Oppublished
      Arabidopsis thaliana DNA chromosome 4, ESSA I FCA contig fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Arabidopsis thaliana"
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/db_xref="texon:3702"
/chromosome="4"
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/clone="BAC TAMU8H22"
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EU Arabidopsis sequencing, project.
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complement(685. .744)
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Arabidopsis thaliana
                                                                                       297336.1 GI:2244788
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Shinn, P. (SSP/Salk) and Seki, M. (RIKEN GSC) contributed equally to this work. Shinozaki, K. (RIKEN GSC) and Ecker, J.R. (SSP/Salk) contributed equally to this work as PIs.
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/product="casein kinase I"
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                                                                                                                                                                                                                                       complement(join(6533. .6772,6888. .7024,7289. .7352,7451. .7524,7658. .7784,7870. .7954,8046. .8109,8216. .8277,8489. .8559,8688. .8783,8860. .9008,9099. .9168,9435. .9475,
                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(join(6533. .6772,6888. .7024,7289. .7352,
7451. .7524,7658. .7784,7870. .7954,8046. .8109,8216. .8277,
8489. .8559,8688. .8783,8860. .9008,9099. .9168,9435. .9475,
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/gene="dl3210c"
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/gene="dl3210c"
6533. .9660
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                                                         6429. .6468
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Eukaryota; Viridipantae; Streptophyta; Embryophyta; Tracheophyta; Bukaryota; Viridipantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyjedons; core eudicots; Rosidae; eurosids II: Brassicales; Brassicaceae; Arabidopsia.

1 (Dases I to 1161)
Shinn, P., Chen, H., Cheuk, R., Kim, C.J., Koesema, E., Meyers, M.C., Banh, J., Bowser, L., Carninci, P., Chang, E., Dalle, J.M., Goldsmith, A.D., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Lam, B., Lee, J.M., Lin, J., Miranda, M., Ondders, C.S., Palm, C.J., Quedch, H.L., Sakurai, T., Arabidopsis, C.S., Toriumi, M., Arabidopsis, ChNA, clones
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PLN 19-DEC-2001
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Shinn, P., Chenk, R., Kim, C.J., Koesema, E., Meyers, M.C.,
Shinn, P., Chen, H., Cheuk, R., Kim, C.J., Koesema, E., Meyers, M.C.,
Banh, J., Bowser, L., Carninci, P., Chang, E., Dale, J.M.,
Goldsmith, A.D., Hayashizaki, Y., 1shida, J., Jones, T., Kamiya, A.,
Karlin Neumann, G., Kawai, J., Lam, B., Lee, J.M., Lin, J., Miranda, M.,
Narusaka, M., Nguyen, M., Onodera, C.S., Pallm, C.J., Quach, H.L.,
Sakurai, T., Satou, M., Seki, M., Southwick, A., Tang, C.C., Toriumi, M.,
Wu, H.C., Yamamura, Y., Yu, G., Yu, S., Shinozaki, K.,
Dariect Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (09-NOV-2001) Salk Institute Genomic Analysis Laboratory (SIGNAL), Plant Biology Laboratory, The Salk Institute for Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL cDNA : 'RIKEN Arabidopsis Full-Length cDNA') : Seki,M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J., Hayashizaki,Y. and Shinozaki,K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The Salk, Stanford, PGEC (SSP) Consortium members carried out the sequencing and annotation of the RAFL cDNAs: Shinn,P., Chen,H., Cheuk,R., Kim,C.J., Koesema,E., Meyers,M.C., Banh,J. Bowser,L., Chang,E., Dale,J.M., Goldsnith,A.D., Jones,T., Karlin-Neumann,G., Balm,C.J., Quach,H.L., Southwick,A., Tang,C.C., Toriumi,M., Wu,H.C., Yamada,K., Yamamura, Y., Yu,G., Yu,S., Davis,R.,,
                                       521 gtaggagggaatgtggctggttcgttaattgcttcgggaccggtagtgttgatggctgct 580
401 gigattaccetgcatggtcggtttgacattttgtctttgaccggtactgcgcttccaccg 460
                                                                                                                                                                  461 cctgcaccaccgggagcaggagtttgacggtgtatctagccggaggtcaaggacaagtt
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Arabidopsis thaliana AT4g17800/d14935c mRNA, complete cds.
AF446359
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/organism="Arabidopsis thaliana"
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complement(join(8240. .8764,8837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="hypothetical protein"
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                                                                                                                                   2 (bases 1 to 81835)
EU Arabidopsis sequencing, project.
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/db_xref="taxon:3702"
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/gene="d14875c"
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/gene="d14875c"
8240. 9391
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/gene="d14875c"
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      REFERENCE
                      AUTHORS
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                                                                                                                                                          AUTHORS
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                                                                                                                                                                                                                                                                                                                COMMENT
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RESAMTLRAILLEYINGCDVFDCVATTARRQGGCVCGGCTVINVSIRQPSAGAV
VTLQGTFEILSLGSSFLPPPAPPGATSLTIFLAGGGGVVGGSVVGELTAAGPVIVIA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1;
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No. 9.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              458 ccgcctgcaccaccgggagcaggaggtttgacggtgtatctagccggaggtcaaggacaa 517
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      385 GATGTTTCGACTGCGTTGCGACTTATGCTCGTCGGAGACAGCGAGGGATCTGCGTTCTG 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     398 ggtgtgattaccctgcatggtcggtttgacattttgtctttgaccggtactgcgcttcca 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  619 GTGGTTGGAGGAAGCGTTGTGGGTGAGCTTACGGCGGCTGGACCGGTGATTGTGATTGCA 678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             325 ATCACGCGCGAGAGCGCAAACACTCTAAGAGCTCACATTCTTGAAGTAACAAACGGCTGC 384
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  19.5%; Score 190.4; DB 8; Length 1161; 64.5%; Pred. No. 9.3e-43; tive 0; Mismatches 161; Indels 6;
                                                                                                                                                              /note="probable AT-hook DNA-binding protein"
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                                            /organism="Arabidopsis thaliana"/db_xref="taxon:3702"
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/note="ecotype: Columbia"
                                                                                                                                                                                                /product="AT4g17800/d14935c"
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              FEATURES
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/translation="MAIQAQHPSRFFFNNSNQQEASDCSLQPODTPFTNFTKAGVDSR
KRSREVYSSALMNPPPPKPSQVIDTTELLQKTPNVVSTGILALFHDOSQNQQPFSSLP
BODTGSK TRORDELDRFTQTGGEELRRFTLADNRERRYVELLCAAESIVGRKLRKKEAE
LEKAPRRHAELEANYMAHVEDARNWQLRAAFREAEVSSLHAHLQQALANRLDTAAKQS
TFGEDGGDAEEAEDAESVYVDPERIELIGPSCRICRRKSATWMALPCQHLILCNGCDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Biochemie, Am Klopferspitz 18a, D-82152 Martinsried, FRG, E-mail: schuelle@mips.biochem.mpg.de,mayer@mips.biochem.mpg.de Project Coordinator: Mike Bevan, Molecular Genetics Department, Cambridge Laboratory, John Innes Centre, Colney Lane, NR4 7UJ Norwich, UK, E-mail: michael. bevan@bbsrc.ac.uk
On Jun 30, 1999 this sequence version replaced gi:2245126.
Information on performance of analysis and a more detailed annotation of this entry and other sequences of chromosomes 3, 4 and 5 can be viewed at: http://www.mips.biochem.mpg.de/proj/thal/this fragment has an overlap with ATFCA8 at the 5' end.
Bevan, M., Stiekema, W., Murphy, G., Wambutt, R., Pohl, T., Terryn, N., Kreis, M., Kavanagh, T., Entian, K.D., Rieger, M., James, R., Puldomenech, P., Hatzopoulos, P., Obermaier, B., Duesterhoft, A., Jones, J., Palme, K., Ansorge, W., Delseny, M., Bancroft, I., Mewes, H.W., Schueller, C. and Chalwatzis, N.
                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (25-JUN-1999) MIPS, at the Max-Planck-Institut fuer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .8764,8837. .9087,9167. .9237,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(join(8240. .8764,8837. .9087,9167. .9237,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="weak similarity to Mus musculus IAP(inhibit apoptosis) homolog A (MIHA) mRNA"
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/translation="Mattrees color of the color of
                                                                                                                                                                                                                                                      complement(join(21664 . .22032,22287 . .22522,22587 . .22923, 23083 . .23181,23268 . .23627,23704 . .23856,24004 . .24131, 2429 . .24392,24476 . .24625))
2429 . .24685
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(join(21664. .22032,22287. .22522,22587. .22923,
23083. .23181,23268. .23627,23704. .23856,24004. .24121,
24229. .24392,24476. .24625))
/gene="di4890c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61524 GGTCGTCGTCCACGTGGCAGACCACCGGGATCCAAGAACAAAACCTCCGGTAATT 61465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="similarity to homeotic protein GL2, Arabidopsis thaliana"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61404 GAIGITITCGACIGCGTIGCGACTIAIGCICGICGGAGACAGCGAGGGAICIGCGIICIG 61345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61290 GCGGTTGTGACGCTACAAGGAACGTTCGAGATTCTTTCTCCCGGATCGTTTCTTCCT 61231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61230 CCTCCGGCACCTCCCGGAGCAACGAGTTTGACAATTTTCTTAGCCGGAGGACAAGGTCAG 61171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61344 AGCGGTAGCGGAACGGTCACGAACGTCAGCATACGTCA-----GCCATCTGCGGCTGGA 61291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             218 ataactagagatagteetaaegteettagateacaegttettgaagteaeeteeggtteg 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gacatatccgaggcagtctccacctacgccactcgtcgcggctgcggcgtttgcattata 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           338 agcggcacgggtgcggtcactaacgtcacgatacggcaacctgcgggctccggctggtgga 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ggtgtgattaccctgcatggtcggtttgacattttgtctttgaccggtactgcgcttcca 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     458 ccgcctgcaccaccgggagcaggaggtttgacggtgtatctagccggaggtcaaggacaa 517
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
19.5%; Score 190.4; DB 8; Length 81835;
Best Local Similarity 64.5%; Pred. No. 1.4e-42;
Matches 303; Conservative 0; Mismatches 161; Indels 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product-"GLABRA2 like protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref-"SPTREMBL:023611"
                                                                                                                                                                            complement(21664. .22032)
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                                                                                 21627. .22020
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                    /gene="d14885w"
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                                                      /number=5
                                                                                                                                                                                                                                            /number=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              join(19659. 19700,19880. .20074,20118. .20348,20653. .20742,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note-"weak similarity to T08All.2, Caenorhabditis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /number=1
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17958. .17983
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19659. .22020
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966. .9988
note="23bp T tandem repeat"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /number-2
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20941. .21626
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   repeat_region
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DEFINITION

Locus

g

g δλ ACCESSION VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE AUTHORS JOURNAL REFERENCE AUTHORS JOURNAL

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HIVE BARMGTHKYNMTOVKNISPLYYICSSSCNRGTNLOLGSVEKYNYRSPRYYSAF
YITLIAKDPDACNSLYTFQTRVVEEGFNWTKLSCNIARPKFGPQGKGLGTLYQRYKKS
ELLTHDWIRLYMELAFLKAHLRSPKNPNLSKLYIVWYAIETRONMEPSERLKARNAF
PYLNCDYLPKYPPNLLLITDYVDERGSDTVDSGANTYIDDGDGGKIESFGGNAPODL
YCNSEQARRRTDGTALDTIGWIHWNNRESNGGNWYFRRIFAVHGELNSDGVDGRVHQE
                                                                                                                                                                                                                                                                                                                                                                                                            /note="similarity to T08A11.2, Caenorhabditis elegans
Contains Prokaryotic membrane lipoprotein lipid attachment
site AA67-77"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product-"hypothetical protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(join(16676. 17044,17299. 17534,17599. 17935, 18095. 18193,18280. 18639,18716. 18868,19016. 19133, 19241. 19404,19488. 19637))
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18095. 18193,18280. 18639,18716. 18868,19016. 19133,
19241. 19404,19488. 19637))
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                                                               10054. .10102
12970. .12995
14671. .14712
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Information on performance of analysis and a more detailed annotation of this entry and other sequences of chromosomes 3, 4 and 5 can be viewed at: http://www.mips.blochem.mpg.de/proj/thal/this fragment has an overlap with ATCHRIV46 at the 5' end and an overlap with ATCHRIV48 at the 3' end.

Location/Qualifiers

rce

1. 198067
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KRIDFLANGVPDMLSIFKKNGFTLKEPSLALSGGHTJGFBTGRESNRT FPKVDPELNA
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RPFVELYANNOTAFFEDFARAMEKLGRVGVKGEKDGEVRRCDHFNKLNN"
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TVTPKQGQQPTTAAGTLRLFFHDCFMEGCDASVLIATNSFNKAERDDDLNESLPGDAF
                                                                                                                                                                                                                                                                                                                                                                   PLN 16-MAR-2000
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Mayer,K.F.X.
Unpublished
       61170 GTGGTTGGAGGAAGCGTTGTGGGTGAGCTTACGGCGGCTGGACCGGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGTGATTGATTGTGATTGATTGTGATTGATTGTGATTGATTGATTGTGATTGATTGATTGATTGATTGATTGATTGATTGATTGATTGATTGATTGATTGATTGATTGATTGATTGATTGATTGATTGATTGATTGATTGATTGATTGATTGATTGATTGATTGATTGATTGATTGATTGATTGATTGATTGATTGATTGATTGATTGATTGATTGATTGATTGATTGATTGATTGATTGATTGATTGATTGATTGATTGATTGATTGATTGATTGATTGATTGATTGATTGATTGATTGATTGATTGATTGATTGATTGATTGATTGATTGATTGATTGATTGATTGATTGATTGATTGATTGATTGATTGATTGATTGATTGATTGATTGATTGATTGATTGATTGATTGATTGATTGATTGATTGATTGATTGATTGATTGATTGATTGATTGATTGATTGATTGATTGATTGATTGATTGATTGATTGATTGATTGATTGATTGATTGATTGATTGATTGATTGATTGATTGATTGATTGATTGATTGATTGATTGATTGATTGATTGATTGATTGATTGATTGATTGATTGATTGATTG
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/gene="AT4417690"
/note="strop similarity to peroxidase (EC 1.11.1.7),
/Addicago sativa
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/protein_id="CAB78772.1"
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EU Arabidopsis sequencing, project.
Direct Submission
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/gene="AT4917690"
6476. .7456
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Arabidopsis thaliana
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ATCHRIV47/c
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AUTHORS TITLE JOURNAL

gene

FEATURES

COMMENT

CDS

REFERENCE AUTHORS

JOURNAL REFERENCE • exon

ataactagagatagtectaaegteettagateaeaegttettgaagteaeeteeggtteg 277

218

56416 GAIGITITCGACTGCGTTGCGACTTATGCTCGTCGGAGGAACAGGGATCTGCGTTCTG 56357

278 gacatatecgaggcagtetecacetacgccactegtegeggetgeggegtttgcattata 337

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398 ggtgtgattaccctgcatggtcggtttgacattttgtctttgaccggtactgcgcttcca

518 gttgtaggaatgtggctggttcgttaattgcttcgggaccggtagtgttgatggct 577

517

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FPY IFPKEEY EVMSK IESGSGKSTGSGHDPVENTA IEOEPPAAKKRYHRHTASOLOO
MAELFKEMHEPDTKTRALSKKLGLSPIOVKPWFONRRTOIRAOGSRSDNAKLKAENE
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MKNNNDNMLIAEEEKA IDMELAVSCARELAKMCDINEPLWNKRLDNESVCLNEEETK
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COMPLEMENT LSTVSVINHRICATVNRITSALVNDVGN"
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19.5%; Score 190.4; DB 8;
Best Local Similarity 64.5%; Pred. No. 1.5e-42;
Matches 303; Conservative 0; Mismatches 161;
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ATT12H17 89350 bp DNA 11near PLN 03-FEB-1998
Arabidopsis thallana DNA chromosome 4, BAC clone T12H17 (ESSAII
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Bevan, M., Hilbert, H., Braun, M., Holzer, E., Brandt, A., Duesterhoeft, A., Bancroft, I., Mewes, H.W., Mayer, K. and Schueller, C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
Submitted (03-FEB-1998) MIPS, at the Max-Planck-Institut fuer
Submitted (03-FEB-1998) MIPS, at the Max-Planck-Institut fuer
Biochemia-, Am Klopferspitz 18a, D-82152 Martinsried, FRG, Project
Coordinator: Mike Bevan, Molecular Genetics Department, Cambridge
Laboratory, John Innes Centre, Colney Lane, NR4 7UJ Norwich, UK,
E-mail: michael.bevan@bbsrc.ac.uk
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TITLE
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KEYWORDS
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Human foetal liver Probe #12387 for g

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AAD05839 standard; cDNA; 974 BP 31-JUL-2001 (first entry) AAD05839; RESULT AAD05839

Transcription factor; trait modification; structural characteristic; developmental characteristic; gene therapy; agricultural biotechnology; Arabidopsis thaliana transcription factor G1073 cDNA.

Arabidopsis thallana.

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Query Match Length DB

Score

Result

100.0

/SIDS5/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*

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(MEND-) MENDEL BIOTECHNOLOGY INC.

Nucleotide sequenc A. thaliana transc Arabidopsis thalia Arabidopsis thalia Arabidopsis thalia Arabidopsis thalia Arabidopsis thalia Arabidopsis coun a

AAD06672 AAC48248 AAC46844 AAC42265 AAC39286 AAC51552 AAC51552

1307 1310 1097 1192 1190

191.6 190.4 179.2 178.8 178.8

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26456786

Arabidopsis thalia

AAD05839 AAF80408

Description

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Transcription factor; flowering time; transgenic plant; vernalisation; plant development; plant physiology; flowering; ss.
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            gcagcagccggaggcgtctcagtcgtcggaggttacggggagtggggcccaggcgtgtga
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  plant's traits. The transcription factors are also used in gene therapy.
                                                                                                                                                                                                                      useful
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                                                                                                                                   Reuber L, Keddie J, Ratcliffe O, Heard J,
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KEDDIE J.
RATCLIFFE O.
HEARD J.
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                                                                                                                                                                                      The present sequence encodes a plant transcription factor protein which modifies the flowering time of a plant. The polynucleotide sequence is used to produce transgenic plants which have a modified flowering time or a modified vernalisation requirement. The polynucleotides and polypeptides are useful for modifying plant development, physiology or biochemistry such that the modified plants have a trait advantage over wild type plants. In particular they are useful for accelerating, delaying or preventing flowering. The polynucleotides are also useful as nucleic acid probes and primers. They may be used to identify proteins that can modify the activity of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           360
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                                                                                                                         New transgenic plant comprises a recombinant polynucleotide encoding plant transcription factor polypeptide and has a modified flowering time or vernalization requirement - \,
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                                                                Samaha
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                             (REUB/) REUBER L. (RIEC/) RIECHMANN J L.
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 CREELMAN R.
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Plant transcription factor; phenotype; sugar sensing characteristic; transgenic plant; plant yield; growth; germination; photosyntheels; glyoxylate metabolism; respiration; pathogen response; wounding response; cell cycle regulation; pigmentation; flowering; senescence; physiology;
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17-APR-2000; 2000US-0197899.
22-AUG-2000; 2000US-0227439.
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PILGRIM M.
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HEARD J.
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(PILG/)
(ADAM/)
(RIEC/)
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Thu Jul 11 11:00:58 2002

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YUNGS() YU G.

YUNGS() YU G.

YU G. Samaha R.

PFDDB: AAE02571.

PROPED REPORT: 2001-135977/35.

PPSDB: AAE02571.

Nucleic acids encoding plant transcription factor polypeptides, useful for a learing the sugar sensing characteristics of plants and increasing relad, e.g. corn, potato and cotton plants -

Yield, e.g. corn, potato and cotton plants -

You patent relates to polynucleotides encoding 35 plant transcription

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Claim 4; Page 143-144; 151pp; English.

C. Gevering and characteristics and increasing yield when their expression care central regulatory molecules that control aspects of plants, photosynthesis, qiyoxylate metabolism, crespination, starch and sucrose synthesis and degradation, pathogen respination, starch and sucrose synthesis and depracation, pathogen control for seaponse, cell cycle regulation plants in seeds, tubers, rocts, and other storage organs leading to an increase in yield. The transcription factor polynucleotides and conscription factor consumber, eggplant, grapes, honey dew, lettuce, mango, melon, conton, papaya, peas, peppers, pineapple, spinach, squash, sweet corn, conton, papaya, peas, peppers, pineapple, spinach, squash, sweet corn, conton, papaya, peas, peppers, pineapple, spinach, squash, sweet corn, choncon, charter condon, papaya, pe
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                                                                            351 aagaaggecaagaggaagaccagcaggatecaagaacaaacetaaagetecaataateat 410
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Query Match
20.2%; Score 196.8; DB 22; Length 1020;
Best Local Similarity 64.6%; Pred. No. 4.6e-52;
Matches 310; Conservative 0; Mismatches 167; Indels 3;
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Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
                                                                                Arabidopsis thaliana DNA fragment SEQ ID NO: 56797.
                                         AAC48248 standard; DNA; 1307 BP
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PR 18-JUN-1999, 9908-0133461.
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PR 24-JUN-1999, 9908-0140335.
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PR 23-JUN-1999, 9908-0144333.
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PR 23-JUN-1999, 9908-0144333.
PR 23-JUN-1999, 9908-0144333.
PR 23-
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   281 atatccgaggcagtctccacctacgccactcgtcgcggctgcggcgtttgcattataagc 340
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                                                                                                                                                  Arabidopsis thaliana DNA fragment SEQ ID NO: 51614.
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

July 10, 2002, 22:14:33 ; Search time 56.06 Seconds (without alignments) 462.792 Million cell updates/sec Run on:

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2: pir2:*
3: pir3:*
1: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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eft, A.; Hoheis

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RESULT

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schuelle@mips.biochem.mpg.de,mayer@mips.biochem.mpg.de Project Coordinator: Mike Bevan, Molecular Genetics Department, Cambridge Laboratorry, John Innes Centre, Colney Lane, NR4 7UJ Norwich, UK, E-mail: michael.bevan@bbsrc.ac.uk
Information on performance of analysis and a more detailed annotation of this entry and other sequences of chromosomes 3, 4 and 5 can be viewed at: http://www.mips.biochem.mpg.de/proj/thal/.
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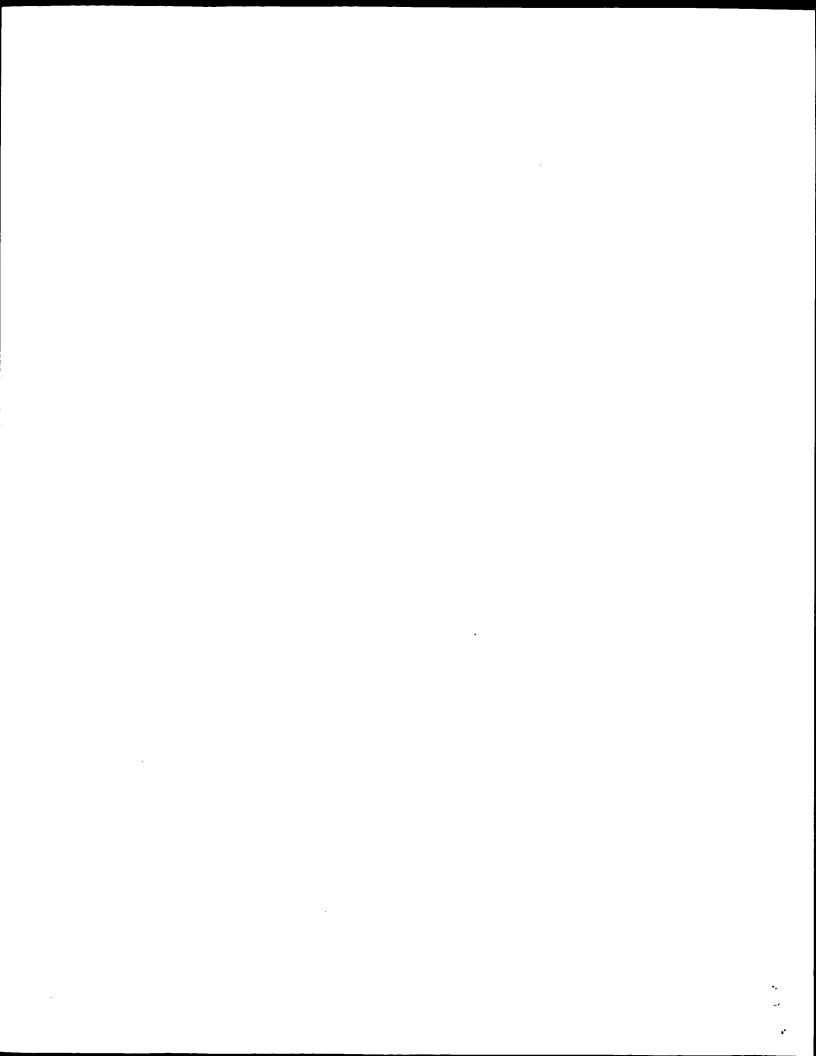
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Arabidopsis thaliana DNA chromosome 4, contig fragment No. 83.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Epermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 16641 to 103350)
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EU Arabidopsis sequencing, project.

BIO Arabidopsis sequencing, project.

Direct Submission
Submitted (10-MAR-2000) MIPS, at the Max-Planck-Institut fuer
Biochemie, Am Klopferspitz 18a, D-82152 Martinsried, FRG, E-mail:
Biochemips blochem.mpg.de project
Coordinator: Mike Bevan, Molecular Genetics Department, Cambridge
Laboratory, John Innes Centre, Colney Lane, NR4 7UJ Norwich, UK,
Engl: michael. Bevan@bbsrc.ac.uk
Information on performance of analysis and a more detailed
annotation of this entry and other sequences of chromosomes 3, 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Robben, J., Grymonprez, B., Volckaert, G., Mewes, H.W., Lemcke, K. and
Mayer, K.F.X.
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Unpublished
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8560 AATTGCTTCGGGACCGGTAGTGTTGATGGCTGCTTCTTTTGCAAACGCAGTTTATGATAG
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                                                                                                                                                                                                                                 Rose, M., Hempel, S., Entlan, K.-D., Mewes, H.W., Lemcke, K.
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July 10, 2002, 22:19:08; Search time 103.68 Seconds (without alignments) 450.508 Million cell updates/sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	-	Q9s7c9 arabidopsis	023620 arabidopsis			022130 arabidopsis	Q9sz70 arabidopsis	082166 arabidopsis	O49662 arabidopsis	Q9lzx7 arabidopsis		Q9sjg4 arabidopsis	Q9lta2 arabidopsis	Q9m9r4 arabidopsis	-	Q9lvb0 arabidopsis
QI	065489	Q9S7C9	023620	Q9C9K7	09SR17	022130	095270	082166	049662	09L2X7	09M2S3	Q9SJG4	Q9LTA2	Q9M9R4	Q941Y9	09LVB0
!	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10
% Query Match Length DB	270	311	292	302	315	317	339	285	324	265	310	257	276	206	265	404
% Query Match	100.0	50.8	46.4	46.4	45.8	45.2	44	44.3	43.5	41.7	41.1	39.8	35.9	30.0	29.5	20.8
Score	1392	706.5	646.5	645.5	637.5	629.5	625.5	616	505	581	572	554	499.5	417	407	289.5
Result No.	-	8	m	4	· LCI	œ	, -	· oc	σ	10	11	12	13	14	15	16

Q9xhy4 oryza sativ Q9aym0 oryza sativ		n			Q9sh33 arabidopsis										-		Q9sr16 arabidopsis		Q9m2d3 arabidopsis	Q9sjq2 arabidopsis	ס	Q23057 caenorhabd1		Q9gub5 galleria me	O	3212	Q92kq8 rhizobium m
Q9XHY4 O9AYM0	094F52	022812	023142	Q9FHM5	Q9SH33	092RR7	049658	Q9FIR1	004696	049350	094010	004695	09SB31	049694	098273	080834	09SR16	081321	09M2D3	098302	09V889	023057	Q9N1P0	Q9GUB5	023347	053212	Q92KQ8
21	101	10	10	10	10	10	10	10	10	10	10	10	101	10	10	10	101	10	10	10	'n	'n	9			9	9
771	351	296	351	419	826	300	334	386	347	439	439	334	404	455	365	348	418	345	348	574	848	405	818	1468	265	694	1610
20.8	20.3	19.7	19.7	19.0	18.6	18.6	18.4	17.9	17.7	17.5	17.5	17.4	17.2	17.2	16.3	16.2	15.9	15.7	15.2	11.7	10.6	10.5	10.3		6.6	8.6	
289	282	274	274	264.5	259	258.5	255.5	248.5	246.5	243	243	242.5	239.5	239	227	225	223	218	211.5	162.5	148	146	143.5	139	138.5	137	136.5
17	13	20	22	22	23	200		26	27	200	800	9.6	S E	3.5	1 c	3.4	. 6	3.6	3.7	. 6	3 6	0.4		42		44	4.5

ALIGNMENTS

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BEVAN M., Hilbert H., Braun M., Holzer E., Brandt A., Duesterhoeft A.,
Bevan M., Hilbert H., Heijnen L., Vos P., Mewes H.W., Mayer K.F.X.,
Hohelser C.;
Schueller C.;
Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
                                               01-MC-1998 (TrEMBLrel. 07, Created)
01-MC-1998 (TrEMBLrel. 07, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL SC.8 KDA PROTEIN.
F23E12.50 CR AT4G53390.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Eukaryota; Viridiplantae; Streptophyta; eudioctyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Best Local Similarity 100.0%; Score 1392; DB 10; Length 270;
Best Local Similarity 100.0%; Pred. No. 4.7e-88;
Matches 270; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                       Hilbert H., Braun M., Holzer E., Brandt A., Duesterhoeft A., Mewes H.W., Lemcke K., Mayer K.F.X.; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AL022604; CAA18730.1; -
EMBL; AL161587; CAB80256.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein.
SEQUENCE 270 AA; 26774 MW; 4C21487C2719E114 CRC64;
                            PRT; 270 AA.
                                  PRELIMINARY;
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SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
                                065489
RESULT
065489
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MEDINE-9812113; PubMed-9461215;

A MEDLINE-9812113; PubMed-9461215;

Bevan M., Bancroft I., Bent E., Love K., Goodman H., Dean C.,

Bevan M., Bancroft I., Bent E., Love K., Goodman H., Dean C.,

Bevan M., Dancs K., Dirkse W., Van Stavera M., Elekema W., Drost L.,

Ridley P., Hudson S.A., Patel K., Murphy G., Piffanelli P., Wedler H.,

Redler E., Wambutt R., Weltzenegger T., Pohl T.M., Terryn N.,

Redler E., Wambutt R., Weltzenegger T., Pohl T.M., Terryn N.,

A duborg S., Gy I., Kreis M., Loo Clerck R., van Montegu M., Lecharny A.,

Britan K.D., Rieger M., Echer P., Punk B., Mueller Auer S.,

Silvey M., James R., Montfort A., Pons A., Pulgdomenech P., Douka A.,

Voukelatou E., Milioni D., Hatzopoulos P., Piravandi E., Obermaler B.,

Rahlbert H., Duesterhoft A., Moores T., Jones J.D.G., Eneva T.,

Rahlme K., Benes V., Rechman S., Ansorge W., Cooke R., Berger C.,

Rahlesny M., Voet M., Volckaert G., Mewes H.M., Klosterman S.,

Rahlysis of I., Mb of contiguous sequence from chromosome 4 of
                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62 GGSGSSGGGGGGGGGGCVVGRRPRGRPPGSKNKPKPPVIIIRESANTLRAHILEVINGCD 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     74 ISEAVSTYATRRGCGVCIISGTGAVTNVTIRQPAAPAGGGVITLHGRFDILSLTGTALPP 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 134 PAPPGAGGLTVYLAGGQGQVVGGNVAGSLIASGPVVLMAASFANAVYDRLPIEEEETPPP 193
                                                        180 YDRLPIEEEETP-----PPRTTGVQQQPEASQSSEVTGSGAQACESNLQGGNG 228
                                                                                             239 FERLPIEEEEEEGGGGGGGGGGGGPPQ----MQQAPSASPPSGVTGQGQ------LGGNV 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              194 RTTGVQQQQPEASQSSEVTGSGAQACESNLQGGN------GGGGVAFYNLGMNMN-NF 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19 GGATSSATASGSSS-----GRRPRGRPAGSKNKPKPPTIITRDSPNVLRSHVLEVTSGSD 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 292;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     47; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; 297344; CAB10560.1; -.
EMBL, ALL61547; CAB78783.1; -.
Hypothetical protein.
SEQUENCE 292 AA; 29724 MW; 2A948700FA543C4F CRC64;
                                                                                                                                   229 GGGVAFYNLGMNMNNFQFSGGDIYGMSGGS---GGGGGGATRPAF 270
                                                                                                                                                                       -----YGFSGDPHLLGWGAGTPSRPPF 311
                                                                                                                                                                                                                                                                                                                         01-JAN-1998 (TrEMBLrel. 05, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update) HYPOTHETICAL 29.7 KDA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 10;
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52.7%; Pred. No. 5.9e-37;
iive 32; Mismatches 47
                                                                                                                                                                                                                                                                        292 AA
                                                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis thaliana (Mouse-ear cress).
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                                                                                                                                                                                                                                                                        PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 391:485-488(1998).
                                                                                                                                                                                                                                                                        PRELIMINARY;
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=3702;
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                                                                                                                                                                                                                                                                                                                                                                                          AT4G17800
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                                                                                                                                                                                                                              121 FDILSLIGTALPPPAPPGAGGLIVYLAGGQGQVVGGNVAGSLIASGPVVLMAASFANAVY 180
                                                                                                                                                                         Arabidopsis thaliana (Mouse-ear cress).
Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta:
Spermatophyta: Magnoliophyta: eudicotyledons: core eudicots: Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67 EVTSGSDISEAVSTYATRRGCGVCIISGTGAVTNVTIRQPAAP-----AGGGVITLHG 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          120 RFDILSLTGTALPPPAPPGAGGLTVYLAGGQGQVVGGNVAGSLIASGPVVLMAASFANAV 179
                                                                            61 LRSHVLEVTSGSDISEAVSTYATRRGCGVCIISGTGAVTNVTIRQPAAPAGGGVITLHGR 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Weigel D., Ahn J.H., Blazquez M.A., Borevitz J., Christensen S.K., Fankhauser C., Ferrandiz C., Kardailsky I., Neff M.M., Nguyen J.T., Sato S., Wang Z., Xia Y., Dixon R.A., Harrison M.J., Lamb C.J., Yanofsky M.F., Chory J.; "Activation Tagging in Arabidopsis."; "Activation Tagging in Arabidopsis."; Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
  1 MELNRSEADEAKAETTPTGGATSSATASGSSSGRRPRGRPAGSKNKPKPPTIITRDSPNV
                      1 MELNRSEADEAKAETTPTGGATSSATASGSSSGRRPRGRPAGSKNKPKPPTIITRDSPNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEGERSPIEL N.A. Palm C.J., Conway A.B., Conn L., Hansen N.F., Altafil H., Araujo R., Huizar L., Rowley D., Buchler E., Dunn P., Gonzalez A., Kremenerskaia I., Kim C., Lenz C., Li J., Liu S., Luros S., Schwartz J., Shinn P., Toriumi M., Vysotskaia V.S., Walker M., Yu G., Ecker J., Theologis A., Davis R.W.; EMBL, AF1999) to the EMBL/GenBank/DDBJ databases.

EMBL, AC007369; AAD30602.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 311;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            %; Pred. No. 5e-41;
25; Mismatches 56; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 311 AA; 31842 MW; A80B445C9776EB7D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50.8%; Score 706.5; DB 10; 53.0%; Pred. No. 5e-41;
                                                                                                                                                                                                                                                                                                                               241 MNNFQFSGGDIYGMSGGSGGGGGGATRPAF 270
                                                                                                                                                                                                                                                                                                           241 MNNFQFSGGDIYGMSGGSGGGGGGATRPAF 270
                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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Pfam; PF02178; AT_hook; 1.
SMART; SM00384; AT_hook; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

July 10, 2002, 22:14:33 ; Search time 56.06 Seconds (without alignments) 462.792 Million cell updates/sec

US-09-823-676-2 1392 1 MELNRSEADEAKAETIPTGG.....IYGMSGGSGGGGGATRPAF 270 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283138 segs, 96089334 residues Searched:

283138 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result								
Š.	Score	Query Match	Query Match Length DB	<u>e</u>	ΩI	Description		Query Match Best Local Simil
1	1392	100.0	270	~	T06118	hypothetical prote		marches 2/0;
7	706.5	50.8	311	N	F86341	hypothetical prote	δŏ	1 MELNRSE
m	646.5	46.4	292	N	C71448	hypothetical prote		
4	645.5	46.4	302	~	Н96792	unknown protein F1	q _Q	-
S	629.5	45.2	317	~	D84890	probable AT-hook D		
ø	625.5	44.9	339	~	T06612	hypothetical prote	ò	61 LRSHVLEN
7	919	44.3	285	~	E84766	probable AT-hook D		
80	605	43.5	324	C)	T04576	hypothetical prote	<u>a</u>	61 I
6	581	41.7	265	~	T47898	hypothetical prote		
10	572	41.1	310	~	T47695	hypothetical prote	Qy	121 FDILSLT
11	554	39.8	257	~	B84860	hypothetical prote		
12	417	30.0	206	~	G86279	Fl4L17.27 protein	d d	121 F
13	274	19.7	296	~	G84747	AT-hook DNA-bindin		
14	255.5	18.4	334	~	T04572	hypothetical prote	Oy	181 DRLPIEE
15	246.5	17.7	347	ď	T06584	probable DNA-bindi		=======================================
16	243	17.5	439	ď	T52291	probable DNA-bindi	<u>අ</u>	181 DRLPIEE
17	239.5	17.2	404	~	T05553	hypothetical prote		
18	239	17.2	455	~	T05081	hypothetical prote	δ	241 N
19	227	16.3	365	~	T06615	hypothetical prote		=======================================
50	225	16.2	348	7	T02462	probable AT-hook D	<u>а</u>	241 MNNFQFS
21	218	15.7	345	7	T01348	hypothetical prote		
22	211.5	15.2	348	~	T47923	probable DNA-bindi		
23	162.5	11.7	574	7	A84782	hypothetical prote	RE	RESULT 2
24	146	10.5	405	~	T29167	hypothetical prote	F8	F86341
22	139	10.0	307	~	T27609	hypothetical prote	hy	hypothetical prote
	137	9.6	694	~	F70868	hypothetical glyci	Ü	C; Species: Arabido
	135.5	7.6	290	~	T23416	hypothetical prote	: :	C;Date: 02-Mar-20(
28	134.5	9.7	839	~	F75518	hypothetical prote	ΰ	C;Accession: F8634
58	131	9.6	388	~	T29173			R:Theologis, A.;

hypothetical glyci protein kinase sag	related to Nup98-N	mucin, submaxillar	hypothetical prote	hypothetical prote	female sterile hom	hypothetical prote	probable deoxyr1bo	gene mastermind pr	CREB-binding prote	hypothetical glyci	regulatory factor	fibroin-3 related	insulin receptor s	hypothetical prote
E70806 S35327	T51890	T03099	T31611	A83412	A43742	D46449	S57795	T13998	T13828	H70589	A35913	T49510	S30185	B64924
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1381	1844	13288	1585	2468	2038	528	867	1655	3190	615	979	670	1231	418
4 m	۳.	6.3	9.5	9.2	0.6	9.0	6.8	6.8	6.8	8.8	8.8	8.7	8.7	8.7
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131 9.			128.5	128	125.5	125	124.5	124				121.5	121.5	121

ALIGNMENTS

ô EVTSGSDISEAVSTYATRRGCGVCIISGTGAVTNVTIRQPAAPAGGGVITLHGR 120 Gaps EADEAKAETTPTGGATSSATASGSSSGRRPRGRPAGSKNKPKPPTIITRDSPNV 60 ö Length 270; Indels 100.0%; Score 1392; DB 2; .larity 100.0%; Pred. No. 6.6e-85; Conservative 0; Mismatches 0;

EEETPPPRITGVOOOPEASOSSEVIGSGAQACESNLQGGNGGGGVAFYNLGMN 240 SGGDIYGMSGGSGGGGGATRPAF 270

tein F9H16.12 - Arabidopsis thaliana dopsis thaliana (mouse-ear cress) 001 #sequence_revision 02-Mar-2001 #text_change 31-Dec-2001 341

Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon

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9905-0134221

9905-0134370

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9905-0135629

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9905-0135629

9905-0135629

9905-013722

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                                                                                                          Score 178.8; DB 21;
Pred. No. 2.8e-46;
0; Mismatches 172;
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99US-0161404.
99US-0161405.
99US-0161359.
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99US-0161360.
99US-0161361.
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63.2%;
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Matches 311; Conservative
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The invention relates to a novel cell cycle protein (CCP) and the CC plynucleotides encoding them. CCP is useful for identifying a compound which bindiates the activity of the polypeptide and which binds to the polypeptide and an anti-CCP antibody is useful for identifying the presence of CCP in a sample. A CCP modulator is useful for modulating the presence cycle or growth of a plant such as Arabidopsis thaliana, rice, wheat, conformation alfalfa, oilseed rape, soybean, sunflower and canola. CC cycle or growth of a plant such as rabidopsis thaliana, rice, wheat, cc CCP nucleic acid and polypeptide molecules are useful as modulating cell cycle progression in plants. CCP is useful as gapnts in regulating cell cycle progression in plants. CCP is useful at cc cc protein or production of CCP protein of production of CCP protein or production of CCP protein forms which have decreased or cc CC plant morphology, blochemistry as herbicides or plant growth regulators. The polymucleotide is useful for modifying cell fate, plant development, plant morphology, blochemistry and/or physiology, the length of the CC stimulation or enhancement of cell cycle of a plant, initiation, promortion, seed size, seed development, theory, fruit, leaf formation, seed size, seed development, module function, dwarfism in plants, seed size, seed development, module function, dwarfism in plants, cc and the anti-CCP antibody are useful in agriculture to modulate the coll cycle of cold, nutrient deprivation, har, drought, salt stress, or blots cc cold, nutrient deprivation, har, drought, salt stress, or blots creases and/or storage organs of plants or the plant architecture, plant quality traits, plant cold stress and attenuate plant architecture, plant quality traits, plant creased the stress and seed development, endoreduplication in storage organs or storage organs or storage organs or storage organs and the modulate cype organized cold, 
                                                                                                                                                                                                                                                     New cell cycle protein and nucleic acid molecule encoding it useful for regulating cell cycle progression in plants and for identifying modulators which are useful as herbicides or plant growth regulators
                                                                                                                                 De Veylder L, Acosta JAT, Magyar Z;
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                          12-MAY-2000; 2000US-204045P.
                                                                              (CROP-) CROPDESIGN NV.
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P-PSDB; AAU72537.
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Sequence 1251 BP; 301 A; 254 C; 335 G; 361 T; 0 other;

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                                                                                                                                                                                                                    273 gitteggacatatecgaggeagtetecacetaegeeaetegtegeggetgeggegttgea 332
                                                                                                                                                                                                                                     ttataagcggcacgggtgcggtcactaacgtcacgatacggcaac----- 377
                                                                                                                                                                                                                                                                                             637 tettgageggaaatggeacagtggetaaegteaeceteegteaaecetegaeegetgeeg 696
                                                                                                                                                                                                                                                                                                                       ---ctgcggctccggctggtggaggtgtgattaccctgcatggtcggtttgacattttgt 434
                                                                                                                                                                                                                                                                                                                                              697 ttgcggcgctcctggtggtggggctgttttggctttacaagggaggtttgagattcttt 756
                                                                                                                                                                                                                                                                                                                                                                                                757 ctitaaccggttctttcttgccaggaccggctccacctggttccaccggtttaacgattt 816
                                                                                                                                                                                                                                                                                                                                                                        435 ctttgaccggtactgcgcttccaccgcctgcaccaccgggagcaggaggtttgacggtgt 494
                                                                                                                                                                                                                                                                                                                                                                                                                          495 atctagccggaggtcaaggacaagttgtaggaggaatgtggctggttcgttaattgctt 554
                                                                                                                                                                                                                                                                                                                                                                                                                                                   817 acttagccggtggtcaaggtcaggttgttggaggaagcgtggtggggccattgatggcag 876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cgggaccggtagtgttgatggctgcttctttgcaaacgcagtttatgataggttaccga 614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACW1; plant cell wall; digestion efficiency; crop; agriculture; ss.
                                                                Score 177.2; DB 21; Length 1303;
Pred. No. 9.6e-46;
0; Mismatches 173; Indels 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA289379 standard; DNA; 12319 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (OJIP ) OJI PAPER CO.
(KAZU-) ZH KAZUSA DNA KENKYUSHO.
            99US-0161992.
99US-0161993.
99US-0162142.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               615 ttgaagaggaagaaacccca 634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       937 tggaggaggaagaagcagca 956
                                                                 tch
al Similarity 61.8%;
309; Conservative
  99US-0161920.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A. thaliana ACW1 genomic DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P-PSDB; AAY51874.
28-OCT-1999;
28-OCT-1999;
28-OCT-1999;
29-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JP2000041685-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-FEB-2000
                                                                Query Match
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This invention describes a novel nucleic acid used for modifying the cell wall components of a plant. The modification is used for the improvement in digestion efficiency of useful crops and feed crops. The DNA is useful in agriculture, industry and gardening. This sequence encodes the Arabidopsis thallana ACWI protein which is described in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                         10791 ACACGIGACACCGACCCTCCTATGAGICCTTACATCCTCGAAGITCCTTCAGGAAACGAC 10732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10731 GTCGTCGAAGCCATCAACCGTTTCTGCCGCCGTAAATCCATCGGAGTCTGCGTCCTTAGT 10672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10611 ACCATAACTTTCCATGGAAAGTTTGATCTCCTCTCCGTCTCCGCAACGTTTCTCCCTTCT 10552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10551 CCGCCTCGTACTTCCTTGTCTCCTCCGTTTCTAACTTCTTCACCGTCTCTCGCTGGA 10492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10491 CCTCAAGGACAAATCATCGGAGGGTTCGTCGCTGGTCCACTTATTCGGCAGGAACAGT 10432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10431 TACGTCATCGCCGCAAGTTTCAACAACCCTTCTTATCACGGGTTACCGGCGGAAGAAGA 10372
                                                                                                                                                                                                                                                                                                                                                                                                                                    221 actagagatagtectaaegteettagateaegttettgaagteaeeteeggtteggae 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         281 atatccgaggcagtctccacctacgccactcgtcgcggctgcggcgtttgcattataagc 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 401 gigattaccitgcatggicggittgacattttgictitgaccggiactgcgcticcaccg 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     461 cc-----tgcaccaccgggagcaggaggtttgacggtgtatctagccgga 505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          506 ggtcaaggacaagttgtaggagggaatgtggcttggttcgttaattgcttcgggaccggta 565
                                                                                                                                                                                                                                                                                                                                          Query Match
13.1%; Score 127.6; DB 21; Length 12319;
Best Local Similarity 54.3%; Pred. No. 2.3e-29;
Matches 290; Conservative 0; Mismatches 229; Indels 15; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                566 gigitgaiggcigcitcititgcaaacgcagittaigaiaggitaccgaitgaagagaa 625
                  Modification of the cell wall components of a plant - useful for improving digestion efficiency of crops and feed crops
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10371 CAAAAACACTCGGGGGGACAGGGAAAGAGGGACAATCTCCGCCGGTCTCT 10318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     626 gaaaccccaccgccgagaaccaccggggtgcagcagcagcagcggaggcgtct 679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
                                                                                                                                                                                                                                                                            Sequence 12319 BP; 3722 A; 2213 C; 2413 G; 3971 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arabidopsis thaliana DNA fragment SEQ ID NO: 42770.
                                                                            Disclosure; Page 14-20; 24pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAC44421 standard; DNA; 1219
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                                                                                                                                                                                                                                       method of the invention.
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990S-0145913.
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990S-0145919.
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990S-014704.
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990S-0153758.
990S-0154018.
990S-0154039.
99US-0142154.
99US-0142055.
99US-0142803.
99US-0142803.
99US-0142920.
99US-0143542.
99US-0143542.
99US-0144085.
99US-0144085.
99US-0144332.
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99US-0145086.
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 01-JUL-1999;
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20-AUG-1999;
20-AUG-1999;
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17-AUG-1999;
   9905-0121825.
9905-012180.
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99US-0141842
                                            25-FEB-2000; 2000EP-0301439
                                                            25-FEB-1999;
05-MAR-1999;
22-MAR-1999;
22-MAR-1999;
22-MAR-1999;
06-APR-1999;
06-APR-1999;
16-APR-1999;
23-APR-1999;
23-APR-1999;
23-APR-1999;
30-APR-1999;
30-APR-1999;
30-APR-1999;
44-MAY-1999;
14-MAY-1999;
14-MAY-1999;
14-MAY-1999;
14-MAY-1999;
16-MAY-1999;
25-MAY-1999;
27-MAY-1999;
21-MAY-1999;
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17-JUN-1999;
18-JUN-1999;
           EP1033405-A2
                           06-SEP-2000
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The present sequence is Arabidopsis thallana transcription factor,

G605 cDNA. The transcription factor is used for altering a plant's

blochemical characteristics. The transcription factor may be used to

alter the structure and developmental characteristics of plants such as

soybean, wheat, corn, potato, cotton, rice, ollseed rape, sunflower,

alfalfa, sugar cane, turf, banana, blackberry, blueberry, strawberry,

raspberry, cartaloupe, carrot, cauliflower, coffee, cucumber, eggplant,

grapes, honey dew, lettuce, mango, melon, onlon, pappa, peas, peppers,

plineapple, spinach, squash, sweet corn, tobacco, tomato, watermelon,

cosaceous fruits and/or vegetable brassicas. Transcription factors are

levels of 1 or more transcription factors can change entire biological

pathways in an organism. Therefore manipulating transcription factor

levels in plants offers great potential in agricultural biotechnology

con modifying a plant's traits. Transcription factor cDNA is useful in
                                                                                Transcription factor; blochemical characteristic; controlling element; structural characteristic; developmental characteristic; gene therapy; agricultural blotechnology; plant trait modification; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acids encoding plant transcription factor polypeptides, useful for altering the blochemical characteristics of plants e.g. corn,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yu G, Adam L, Riechmann JL, Heard J, Samaha R;
Pineda O, Jiang C;
                                                                                                                                                                                                                                                 /*tag= a
/product= "Transcription factor, G605"
                                          Arabidopsis thaliana transcription factor, G605 cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1263 BP; 335 A; 314 C; 274 G; 340 T; 0 other;
                                                                                                                                                                                                     Location/Qualifiers 72..1076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 4; Page 75-76; 127pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (MEND-) MENDEL BIOTECHNOLOGY INC. (CREE/) CREELMAN R.
                                                                                                                                                                                                                                                                                                                                                                                 14-NOV-2000; 2000WO-US31344.
                                                                                                                                                                                                                                                                                                                                                                                                                       17-NOV-1999; 99US-0166228.
17-APR-2000; 2000US-0197899;
22-AUG-2000; 2000US-0227439.
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                                                                                                                                                                 Arabidopsis thaliana.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-335999/35.
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PINEDA O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HEARD J.
SAMAHA R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADAM L.
                                                                                                                                                                                                                                                                                                      WO200136597-A1.
                                                                                                                                                                                                                                                                                                                                          25-MAY-2001
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(PINE/)
(JIAN/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (HEAR/)
(SAMA/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (XDGG/)
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53.4%; Pred. No. 0.013;
tive 0; Mismatches 110; Indels 15; Gaps
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                                                                                                   99US-0156596.
99US-0157117.
99US-0157753.
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99US-0158029.
99US-0158232.
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99US-0161993.
99US-0162142.
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99US-0161405
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13-0cr-1999
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18-0cr-1999
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4.3%; Score 42; DB 22; Length 1263;
53.4%; Pred. No. 0.013;
tive 0; Mismatches 110; Indels 15; Gaps
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26-JUL-1999;
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24.-UN-1999;
29.-UN-1999;
30.-UN-1999;
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22-JUL-1999;
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27-MAY-1999;
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  387 cggctggtggaggtgtgattacctgcatggtcggtttgacattttgtctttgaccggta 446
                                                                  447 ctgcgcttc-----caccgcctgcaccaccgggagcaggaggtttgacggtgtatc 497
    604 tttgcgttttatgcgcaaacggtgtcgtttcgagcgttacacttcgtcagcctgattcat 663
                                      c----tggtggtacattgacctatgagggtcggtttgagatattgtcactatctggaa 717
                                                                                                                                                                                                                                                         Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
                                                                                                                                                                                                                                          Arabidopsis thaliana DNA fragment SEQ ID NO: 22725.
                                                                                                                             558 gaccggtagtgttgatggctgcttcttt 585
                                                                                                                                              838 ctcctattcaagtggttgtaggaacttt 865
                                                                                                                                                                                         AAC38928 standard; DNA; 1387 BP.
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05-MAR-1999;
09-MAR-1999;
23-MAR-1999;
25-MAR-1999;
01-APR-1999;
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16-APR-1999;
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24-MAY-1999;
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14-MAY-1999;
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05-MAY-1999;
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99US-0149929.
99US-0149902.
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990S-0151930
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990S-0155139.
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990S-0155659.
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99US-0158029.
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990S-0159637.
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990S-0160741
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99US-0160981.
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31-AUG-1999;
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29-SEP-1999;
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12-OCT-1999;
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Plant transcription factor; phenotype; sugar sensing characteristic; transgenic plant; plant yield; growth; germination; photosynthesis; glyoxylate metabolism; respiration; pathogen response; wounding response; cell cycle regulation; pigmentation; flowering; senescence; physiology; storage organ; metabolism; ss.
                                                                                                                                                                                         327 tttgcattataagcggcacgggtgcggtcactaacgtcacgatacggcaacctgcggctc 386
                                                                                                                                                                                                                                                                                                      387 cggctggtggaggtgtgattaccctgcatggtcggtttgacattttgtctttgaccggta 446
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                               Ouery Match
4.3%; Score 42; DB 21; Length 1387;
Best Local Similarity 53.4%; Pred. No. 0.014;
Matches 143; Conservative 0; Mismatches 110; Indels 15;
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Samaha R;
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/product= "Transcription factor"
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  99US-0161993.
99US-0162142.
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17-APR-2000; 2000US-0197899.
22-AUG-2000; 2000US-0227439.
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RIECHMANN J L.
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JIANG C.

JIANG C.

JINE/) HERRD J.

(PINE/) PILEDRO O.

A (ADAM) ADAM L.

(RIECHY

(YUGG/) YITCHY

(SAMA)
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28-OCT-1999;
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Yu G, Sa
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WPI; 2001-335977/35. P-PSDB; AAE02551

Nucleic acids encoding plant transcription factor polypeptides, useful for altering the sugar sensing characteristics of plants and increasing yield, e.g. corn, potato and cotton plants -

Claim 4; Page 90-92; 151pp; English.

factors which may be used to modify phenotype associated with a plant's factors which may be used to modify phenotype associated with a plant's sugar sensing characteristics and increasing yield when their expression level is altered. Sugars are central regulatory molecules that control aspects of physiology, metabolism and development. Therefore the cDNAs and proteins of the invention are useful for modifying the growth and and proteins of plants, photosynthesis, altrowthate metabolism, crespination, starch and sucrose synthesis and degradation, pathogen response, wounding response, cell cycle regulation, pigmentation, it cresponse, wounding response, cell cycle regulation, pigmentation, cresponse, wounding response, cell cycle regulation, pigmentation, creationships in seeds, tubers, roots, and other storage organs leading to an increase in yield. The transcription factor polynucleotides and polypeptides may be used to alter the structure and developmental characteristics of plants such as soybean, wheat, corn, potato, cotton, rice, oilseed, sunflower, alfalfa, sugarcane, turf, banana, blackberry, ciec, oilseed, sunflower, alfalfa, sugarcane, turf, banana, blackberry, cofton, papaya, peas, peppers, pineapple, spinach, squash, sweet corn, onlon, papaya, peas, peppers, pineapple, spinach, squash, sweet corn, condto, watermelon, rosaceous fruits and/or vegetable brassicas.

Sequence 1606 BP; 459 A; 376 C; 335 G; 436 T; 0 other;

. 6 11Cn 4.3%; Score 42; DB 22; Length 1606; sal Similarity 47.4%; Pred: No. 0.015; 166; Conservative 0; Mismatches 177. Query Match Best Local Matches

249 cacacgitetigaagicaceteeggiteggacatateegaggeagieteeacetaegeea 308 658 ctcatgtcattgaggttaaaacaggagagagacatagctacgaagatattggcgtttacga 717 δ Dp

309 ctcgtcgccgctgccgctttgcattataagccgcaccggtgccgctcactaacgtcacga 368 718 accaagggccacgcgcaatctgtattctctcagctacaggagctgtaactaatgtgatgc 777 ŏ g

tacggcaacetgcggctccggctggtggaggtgtgattaccctgcatggtcggtttgaca 428 778 ttogtoaagotaacaatagoaatoctactggaactgttaagtatgagggoogatttgaaa 837 369 δλ Ω 429 ttttgtetttgaeeggtaetgegettecaeegge------tgeaecaeegggageag 479 tcatttctctgtcaggttctttcttgaattctgagagtaatggtactgtgaccaaaactg 897 838 qq Q

480 gaggittgacggigtatctagccggaggicaaggacaagtigtaggaggaaigiggcig 539 δ g

540 gttcgttaattgcttcgggaccggtagtgttgatggctgcttctttgca 589 ò

958 gaatgctagtagctggatcacaagtccaggtcattgtgggaagctttgta 1007

Search completed: July 10, 2002, 22:14:29 Job time: 7602 sec

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; CLONE: pT2gpt-F1s
US-08-232-463-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear IMMEDIATE SOURCE:
 FILING DATE:
                                                                                                                                                                                                                               US-08-232-463-14/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE
                                                                                                                                                                                                                                                                                                                                                          STATE: VA
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                                                          July 10, 2002, 19:59:17 ; Search time 63.21 Seconds (without alignments) 3784.955 Million cell updates/sec
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Sequence 8, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 32, Appli
Sequence 32, Appli
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Sequence 324, App
Sequence 320, App
Sequence 1, Appl
Sequence 1, Appli
Sequence 659, App
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                                                                                                                    1 cccccgacctgcctctaca......cgaaatgcgaatattaggtt 974
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Sequence 4,
Sequence 4,
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Sequence 3,
Sequence 3,
Sequence 3,
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                                                                                                                                                                                                                                                                                                                                                                                                                          Description
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                                                                                                                                                                                                                                                                                   1: /cgn2_6/ptodata/2/lna/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/lna/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/lna/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/lna/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/lna/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/lna/pcTUS_COMB.seq:*
      GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-08-976-229-14
US-09-199-637A-322
US-09-199-637A-322
US-09-199-637A-1
US-08-998-416-859
US-08-998-416-859
US-08-458-745-1
US-08-458-745-1
US-08-466-390-4
US-08-466-390-3
US-08-466-390-3
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US-08-079-587-8
US-08-289-747-1
US-08-458-298-1
US-08-642-807A-32
US-08-642-807A-32
                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
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                                                                                                                                                                   383533 seqs, 122816752 residues
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Listing first 45 summaries
                                          - nucleic search, using sw model
                                                                                                                                       IDENTITY_NUC Gapoxt 1.0
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Maximum DB seq length: 2000000000
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                                                                                                   US-09-823-676-1
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Match Length DB
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                                                                                                                                                                                           533 gtggctggttcgttaattgcttcgggaccggtagtgttgatggctgcttcttttgcaaac 592
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                                                                                                                                                                                                                                                                                          593 gcagtttatgataggttaccgattgaagaagaagaaaccccaccgccgagaaccaccggg 652
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APPLICANT: TARTAGLIA, James
APPLICANT: GOBEL, SOCOLT J.
APPLICANT: GOREL, SOCOLT J.
APPLICANT: GETTIG, Russell R.
APPLICANT: PINCUS, Steven E.
APPLICANT: PAOLETI, Enzo
APPLICANT: PACOBS, BETTERM L.
TITLE OF INVENTION: VECTORS HAVING ENHANCED EXPRESSION, AND METHODS OF
                                                                                                 473 ggagcaggaggtttgacggtgtatctagccggaggtcaaggacaagttgtaggaggaat 532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
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       DB 1; Length 7218;
  Query Match 4.6%; Score 44.6; DB 1; Length 7
Best Local Similarity 3.5%; Pred. No. 0.0045;
Matches 14; Conservative 216; Mismatches 165; Indels
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CURRENT APPLICATION NUMBER: US/08/815,809
CURRENT FILING DATE: 1997-03-12
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Patent No. 6004777
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7909 GTAAAATGGTGTTTATTATCCTAGGAGATCTATAAATTATAATATAGATTGTTGTTTTT 7968
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                                                                                                                                                                                                                                         TITLE OF INVENTION: VECTORS HAVING ENHANCED EXPRESSION, AND TITLE OF INVENTION: METHODS OF MAKING AND USES THEREOF NUMBER OF SEQUENCES: 48 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   72; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/816,155B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3.5%; Score 33.8; D
51.7%; Pred. No. 10;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                         FROMMER LAWRENCE & HAUG LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    454310-2990
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12-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                      ; Sequence 8, Application US/08816155B ; Patent No. 5990091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 8, Application US/09079587; Patent No. 6130066; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: KOMALSKI, THOMAS J.
REGISTRATION NUMBER: 32.147
REFERENCE/DOCKET NUMBER: 4543
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-588-0800
TELEPHONE: 212-588-0500
                                                                                                           APPLICANT: TARTAGLIA, JAMES
APPLICANT: COX, WILLIAM I.
APPLICANT: GETTIG, RUSSELL R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                           APPLICANT: MARTINEZ, HECTOR
APPLICANT: PAOLETTI, ENZO
APPLICANT: PINCUS, STEVEN E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS: LENGTH: 19877 base pairs
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
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                                                                                   GENERAL INFORMATION:
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RESULT 3
US-08-816-155B-8
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APPLICANT: COX, WILLIAM I.
APPLICANT: GETTIG, RUSSELL R.
APPLICANT: MARTINEZ, HECTOR
APPLICANT: PAOLETTI, ENZO
APPLICANT: PINCUS, STEVEN E.
TITLE OF INVENTION: VECTORS HAVING ENHANCED EXPRESSION, AND
NUMBER OF SEQUENCES: 48
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APPLICANT: Colgin, Mark
TITLE OF INVENTION: CDNAS Encoding Minor Ampullate Spider
TITLE OF INVENTION: Silk Proteins
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                          ZIP: 10151
CMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/09/079,587
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/816,155
FILING DATE: 12-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: KOWALLSKI, THOMAS J.
REGISTRATION NUMBER: 32,147
REFERENCE/DOCKET NUMBER: 454310-2990
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-588-0800
INFORMATION FOR SEQ ID NO: 8:
                                                                                                                                                                                                         FROMMER LAWRENCE & HAUG LLP
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                                                                                                                                                                                                                          STREET: 745 FIFTH AVENUE
CITY: NEW YORK
STATE: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 19877 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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1388 CACCGTACCCACCATGACCACCTCCAGCTCCTGCACCGCAGCGCTCCTGCTC 1329
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Best Local Similarity 53.9%; Pred. No. 4.4;
Matches 69; Conservative 0; Mismatches 59; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/08458298

Patent No. 575677

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Colgin, Mark
TITLE OF INVENTION: 511k Proteins
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Birch, Stewart, Kolasch & Birch
STREET: P.O. Box 747
CITY: Falls Church
STATE: Viginia
                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIDLE
COMPUTER: IEM PC COMPALIDLE
COMPUTER: IEM PC COMPALIDLE
COMPUTER: IEM PC COMPALIDLE
SOFTWARE: PACHOLIN Release #1.0, Version #1.25
SOFTWARE: PACHOLIN BATA:
APPLICATION NUMBER: US/08/209,747
FLING DATE: 14-MAR-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: MULPHY JT. GGRAID M.
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 1447-104P
TELEPHOM. 703-205-8000
TANDAMATION: COMPANIED M. COMPANIE M. COMPANI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: 183...2675
COTHER INFORMATION: /Product- "N. clavipes minor
COTHER INFORMATION: ampullate silk protein"
US-08-209-747-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Nephila clavipes
TISSUE TYPE: minor ampullate gland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 703-205-8050
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2793 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
Falls Church
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LOCATION: 183..2675
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                                                                                               Virginia
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ORGANISM: Nep
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                                                                                                                                COUNTRY:
                                      CITY: 1
STATE:
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COUNTRY:

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SOFTWARE:
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Patent No. 5736378

GENERAL INFORMATION:
APPLICANT: Blder, John R.
APPLICANT: Talbott, Randy L.
TITLE OF INVENTION: NUCLEOTIDE SEQUENCE AND OPEN READING
TITLE OF INVENTION: FRAMES OF FELINE IMMUNOBEFICIENCY VIRUS (FIV)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 33.6; DB 1; Length 2793; Pred. No. 4.4; 0; Mismatches 59; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HAME/KEY: CDS

LOCATION: 183..2675

COTHER INFORMATION: /product= "N. clavipes minor orner information: ampullate silk protein"

US-08-458-298-1
                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/458,298 FILING DATE: UO-JUN-1995 CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Spensley Horn Jubas & Lubitz
STREET: 1800 Century Park East, Suite 500
CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                          PAPLICATION NUMBER: US 08/209,747
FILING DATE: 14-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Murphy Jr., Gerald M.
REGISTRATION NUMBER: 28/977
REFERENCE/POCKET NUMBER: 1447-104P
TELECHONOISICATION INFORMATION:
TELECHONOIS: 703-205-8000
TELEFAX: 703-205-8050
                                                                                                                                                                                                                                                                                                                                         1447-104P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE TYPE: minor ampullate gland
ZIP: 22040-3487
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nephila clavipes
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Best Local Similarity 53.9%;
Matches 69; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 703-205-8050
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 2793 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nucleic acid
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                      CLASSIFICATION: 530
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: CDNA HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS:
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1950 AGGTGCAGATGCTTACTGTGCAGCTTGATTCACTGGGGCTGCAGCTGCGCCCGC 1891
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51.3%; Pred. No. 8;
tive 0; Mismatches 74; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             join(628..1977, 1869..5240, 5236..5988, 5992
..6222, 6262..8824, 6709..6912)
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/325,547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Persing, D. H.
TITLE OF INVENTION: BCR DETECTION OF BORRELIA
TITLE OF INVENTION: BURGDORFERI
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1890 criccagnricccgaarricirriaccaccri 1859
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                                                                                                                                                                                                                                                                                NAME: Wetherell, Jr., Ph.D., John R. REGISTRATION NUMBER: 31,678
REFERENCE/DOCKET NUMBER: PD-2000
                                                                                                                                                                             CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/759,570
FTLING DATE: 12-SEP-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-642-807A-32/c; Sequence 32, Application US/08642807A; Patent No. 6087097
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                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
TELEFAX: (619) 455-5110
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA (genomic)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              9468 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match 3.4%
Best Local Similarity 51.3%
Matches 78; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nucleic acid
EDNESS: single
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MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Minneapolis
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OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
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IMMEDIATE SOURCE:
CLONE: P
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                                                                                                                                                                FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION:
LOCATION:
US-08-325-547-10
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STATE:
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81 aagcagacgaagcaaaggccgagaccactcccaccggtggagccaccagctcagccacag 140
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STREET: 11 S Meridian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORIGINAL SOURCE:
ORGANISM: Plasmodium yoelii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : 5433 base pairs
nucleic acid
EDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indianapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          46204
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                                                                                                                                                                                                                            US-08-929-329-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-929-329-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTHER INFORMATION: CDC 1551
GTHER INFORMATION: "n" bases at various positions throughout the sequence is OTHER INFORMATION: represent a, t, c or g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     481 aggittgacggigtatctagccggaggicaaggacaagtigtaggagggaaigiggcigg 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     852 AGTTTTTTGCTGTTTACACTAATTGTTAAAGTGGAAGTTTTTGAATCCCATNTTCCAGT 793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      541 ttcgttaattgcttcgggaccggtagtgttgatggctgcttcttttgcaaacgcagttta 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: HITTE, Owen R.
APPLICANT: WITTE, Owen R.
APPLICANT: WENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM TITLE OF INVENTION: TUBERCULOSIS
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
SOFTWARE: PACENTIN Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 3.3%; Score 31.8; DB 4; Length 4403765; Best Local Similarity 56.1%; Pred. No. 52; Matches 60; Conservative 0; Mismatches 47; Indels 0; C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
3.4%; Score 33.4; DB 3; Length 1100;
Best Local Similarity 52.1%; Pred. No. 3.2;
Matches 73; Conservative 0; Mismatches 67; Indels 0
             APPLICATION NUMBER: US/08/642,807A FILING DATE: 03-MAY-1996 CLASSIFICATION: 435 PRIOR APPLICATION DATE: APPLICATION NUMBER: 08/241,496 FILING DATE: 12-MAY-1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                    NAME: Woessner, Warren D
REGISTRATION NUMBER: 30,440
REFERCE/DOCKET NUMBER: 150.127US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-373-6900
TELEFAX: 612-339-3061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/09103840A Patent No. 6294328
                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 32: SEQUENCE CHARACTERISTICS: LENGTH: 1100 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     601 tgataggttaccgattgaag 620
                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: Genomic DNA US-08-642-807A-32
CURRENT APPLICATION DATA:
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0; Gaps

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Db 2441955 ACGCGGGGGGGGGGGGCGAAATCCCAATTCAACGGACGCCGCACGAATCCCCGAGACAG 2441896
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                                                                                                                                                                                                                                                                                                                        APPLICANT: Adams, John H
APPLICANT: Dalton, John P
APPLICANT: Dalton, John P
APPLICANT: Cappe, Stefan
TITLE OF INVENTION: Plasmodium Proteins Useful for Preparing
TITLE OF INVENTION: Vaccine Compositions
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Barnes & Thornburg
                                                                                   Db 2441895 CCGCTGGCTAGTCAGCTGGCCGCGGGGTCAGTCCGCGGGT 2441849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 3.2%; Score 31.6; DB 3; Length 5433; Best Local Similarity 52.2%; Pred. No. 23; Matches 70; Conservative 0; Mismatches 64; Indels 0;
                                                      141 cctctggctcttcctccggacgtcgtccacgtggtcgtcctgcaggt 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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APPLICATION NUMBER: US/08/929,329
                                                                                                                                                                                                                                             ; Sequence 1, Application US/08929329
; Patent No. 6120770
; GENERAL INFORMATION:
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ATTORNEY/AGENT INFORMATION:
NAME: Breen, John P
REGISTRATION NUMBER: 38,833
REFERENCE/POCKET NUMBER: 83591
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317) 231-7745
TELEPHONE: (317) 231-7745
TELEFRAX: (317) 231-7745
TELEFRAX: (317) 231-7745
TELEFRAX: (317) 231-7745
SEQUENCE CHARACTERISTICS:
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Sequence 324, Application US/09199637A Patent No. 6355411 GENERAL INFORMATION:
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Goodman, Howard M.
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                                                                   Ausubel, Frederick
Goodman, Howard M.
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                                                                                                                                                       Tan, Man-Wah
Cao, Hui
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LENGTH: 765
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APPLICANT:
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APPLICANT:
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Best Local Similarity 44.4%; Pred. No. 47;
Matches 127; Conservative 0; Mismatches 159; Indels 0;
                                                                                                                        GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
Parplicant: Welch, Rodney A.
TITLE OF INVENTION: Nucleotide Sequence of Escherichia coli
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APPLICATION DATA:

APPLICATION NUMBER: US 60/031,626 AND US 60/061,953

ATORNEY/AGENT INFORMATION:

NAME: Steffe, Eric K.

REGISTRATION NUMBER: 36,688

REFERENCE/DOCKET NUMBER: 1488.0740002/EKS/CBM

TELECOMMUNICATION INFORMATION:

TELECHMONE: (202) 371-2540

TELEPHONE: (202) 371-2540

TELEFAX: (202) 371-2540

INFORMATION FOR SEQ ID NO: 14:
                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 142
CORRESPONDENCE ADDRESS:
ADDRESSE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
STREET: 1100 New York Ave, N.W., Suite 600
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33 OPERATING SYSTEM: MSDOS version 6.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/976,259
FILING DATE: Herewith
CLASSIFICATION: 536
                                                                                   Sequence 14, Application US/08976259 Patent No. 6316609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 22671 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS: double
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US-00-199-637A-324/c
                                                                                                                                                                                                                                   Patent No. 6316609
                                                                 US-08-976-259-14/c
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                                                                                                                                                                                                                                                                                                                                                          STATE:
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601 tgataggttaccgattgaagaggaagaaccccaccgccgagaaccaccggggtgcagca 660
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Gaps
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Best Local Similarity 45.6%; Pred. No. 10;
Matches 110; Conservative 0; Mismatches 131; Indels
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TITLE OF INVENTION: VIRULENCE-ASSOCIATED NUCLEIC ACID
TITLE OF INVENTION: SEQUENCES AND USES THEREOF
                                                                           APPLICANT: Drenkard, Eliana
APPLICANT: Trongalis, John
TITLE OF INVENTION: VIRULENCE-ASSOCIATED NUCLEIC ACID
TITLE OF INVENTION: SEQUENCES AND USES THEREOF
FILE REPERENCE: 00786/361002
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                                                                                                                                                                                           CURRENT APPLICATION NUMBER: 02/09/199,637A CURRENT FILING DATE: 1998-11-25 PRIOR APPLICATION NUMBER: 60/066,517 PRIOR FILING DATE: 1997-11-25 NUMBER OF SEQ ID NOS: 437 SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 322, Application US/09199637A Patent No. 6355411
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Tan, Man-Wah
Rahme, Laurence G
Mahajan-Miklos, Shalina
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US-09-199-637A-324
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28550 CCAGCGGCAGGAGCGCGCCAGCAGCGGGTCCTGGTCGAAGGAGGACAGGCCTTTGA 28491
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                                                                                                                                                                                                                                                                      481 aggittgacggigiatetetagecggaggicaaggacaagtigiaggagggaaigiggeigg 540
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APPLICANT: CaC, HUL

APPLICANT: TSONGALIS, JOHN

TITLE OF INVENTION: SEQUENCES AND USES THEREOF

TITLE OF INVENTION: SEQUENCES AND USES THEREOF

TITLE OF INVENTION: SEQUENCES AND USES THEREOF

CURRENT PELLORATION NUMBER: US/09/199,637A

CURRENT APPLICATION NUMBER: 05/066,517

PRIOR APPLICATION UNDER: 1998-11-25

NUMBER OF SEQ ID NOS: 437

SOFTWARE: FASTSEQ FOR WINDOWS VERSION 4.0
SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 320, Application US/09199637A Patent No. 6355411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Goodman, Howard M.
Rahme, Laurence G.
Mahajan-Miklos, Shalina
Tan, Man-Wah
Cao, Hui
                                                                                      ; ORGANISM: Pseudomonas aeruginosa
US-09-199-637A-322
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APPLICANT: Goodman, Howard M.
APPLICANT: Rahme, Laurence G.
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US-09-199-637A-320
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1092 tgagctgggggaactcgttgaaggagtcgcgggcggcgccggggtcgcgttggtcatgt 1151
                                                                                                                                                601 tgataggttaccgattgaagaggaagaaaccccaccgccgagaaccaccgggggtgcagca 660
                                                                                                              661 gcagcagccggaggcgtctcagtcggaggttacgggagtgggagtcgggcgtgtga
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3.2%; Score 31.4; DB 4; Length 42235;
Best Local Similarity 45.6%; Pred. No. 71;
Matches 110; Conservative 0; Mismatches 131; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Rahme, Laurence G.
APPLICANT: Mahajan-Miklos, Shalina
APPLICANT: Mahajan-Miklos, Shalina
APPLICANT: Cao, Hui
APPLICANT: Cao, Hui
APPLICANT: Drenkard, Eliana
APPLICANT: Drenkard, Eliana
APPLICANT: STORGALIS, John
TITLE OF INVENTION: VIRULENCE-ASSOCIATED NUCLEIC ACID
FILLE OF INVENTION: SEQUENCES AND USES THEREOF
FILLE OF INVENTION SEQUENCES AND USES THEREOF
FILLE OF INVENTION NUMBER: US/09/199,637A
CURRENT APPLICATION NUMBER: 60/066,517
PRIOR FILLING DATE: 1999-11-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 437
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; LOCATION: (1)...(42235) .
; OTHER INFORMATION: N is any nucleic acid. US-09-199-637A-1
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Goodman, Howard M.
Rahme, Laurence G.
Mahajan-Miklos, Shalina
Tan, Man-Wah
                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 1, Application US/09199637A ; Patent No. 6355411
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Search completed: July 10, 2002, 21:34:24 Job time: 5707 sec

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July 10, 2002, 19:01:07 ; Search time 1926.27 Seconds (without alignments) 6824.606 Million cell updates/sec
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                    OM nucleic - nucleic search, using sw model
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Title:

US-09-823-676-1

Sequence:

1 cccccgacctgcctctaca......cgaaatgcgaatattaggtt 974

Scoring table:

Searched:

13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Maximum DB seq Length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

AWS85780 EST317403 BG583651 EST485403 BH550632 BOGUC18TR AW774484 EST333635 AW574000 EST316591 BG687144 EST508763 BG587531 EST489303 BE203784 EST396460 BH419879 BOGGX69TF BG134451 EST467343 AL366947 MEBALIBIO AW776082 EST335147 BH566718 BOHCV23TR BH596283 BOGBL42TR AW980581 EST391734 BG581882 EST483618 Description SUMMARIES 10 BG581882 9 AW585780 10 BG58651 12 BH550635 9 AW774484 10 BG647144 10 BG587531 9 BE203784 11 BH419879 10 BG134451 11 BH4819879 10 BG134451 12 BH481983 9 AL366947 BH566718 BH596283 AW980581 Query Match Length DB 690 765 671 782 534 765 747 747 618 19.8 19.8 19.8 19.3 19.3 18.3 18.3 17.9 17.9 Score 208.6 206 192.4 190.8 190.8 187.6 179.2 179.2 177.6 177.6 173.4 Result ٠ 9

BM110212 EST557748 AW560824 EST315872 B1321563 saf12907 BF0602777 set37f11.y		ອ _	BH513248 BDHQC93TR AW350603 GM210008B AW774872 EST334023 AW72066B LINEST14h BFDAA270 ESWA37769		£ 4 0 0 4	BE02054 745 804 804 804 804 804 804 804 804 804 804
BM110212 AW560824 B1321563 BF067277 BF999313	-		AAA		BH173434 AV544413 BG881387 T43108 AV422634	
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163.8 158.8 158.8 158.6 158.6	157.8 157.6 156.8 150		139.8 138.4 138.2	137.2 137.2 136.4 129	126.2 125.8 125.6 125.2 123.2	117.4 116.2 115.2
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ALIGNMENTS

BG581882 759 bp mRNA linear EST 11-APR-2001 EST483618 GVN Medicago truncatula cDNA clone pGVN-66K1 5' end, mRNA BG581882 BG581882.1 GI:13596946	Darrel medic. Medicago truncatula Eukaryota, Vilidiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papillonoideae; Tiffolleae;	Truckeyo. 1 (bases 1 to 759) Fedorova,M., Plerson,B.L., Samac,D.A., Vance,C.P., Gantt,G.S., Town,C.D., Van Aken,S., Utterback,T., Cho,J. and Fraser,C.M. ESTS from one month old nitrogen-fixing root nodules of Medicago	Unpublished (2001) Contact: Carroll P. Vance Contact: Carroll P. Vance Department of Agronomy and Plant Genetics University of Minnesota 411 Borlaug Hall, 1991 Upper Buford Circle, St.Paul, MN 55108 USA Tel: 612 625 5715 Fax: 651-649-5058	Email: vance0004@maroon.tc.umn.edu University of Minneaota name: M382944e TIGR sequence name: University of Minneaota name: M382944e TIGR sequence name: Witchofirk More information is available at: http://www.medicago.org Seq primer: Skmod (CTA gAA CTA gtg gAT CC). Location/Qualifiers 1. 759 /organism="Medicago truncatula"	/cultivare genotype A17" /db_xref="taxon:3880" /clone="pGvN-66K1" /clone=lb="GVN" /tissue_type="N2-fixing root nodules" /dev_stage="effective root nodules harvested one month post inoculation with Sinorhizobium mellioti"
RESULT 1 BG581882 LOCUS DEFINITION ACCESSION VERSION	SOURCE	REFERENCE AUTHORS TITLE	JOURNAL	FEATURES SOURCE	

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AWS85780 597 bp mRNA linear EST 07-SEP-2000 EST317403 MHAM Medicago truncatula/Glomus versiforme mixed EST
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Contact: Maria J. Harrison
           Anote—"Vector: piluescript SK-; Site_1: EcoRI; Site_2: Xnoie—"Vector: piluescript SK-; Site_1: EcoRI; Site_2: Xnoi: cDNA was prepared from polyA+ enriched RNA from effective root nodules harvested one month post incoulation with Sinorhizobium meliloti. The CDNA was directionally ligated into the Uni-ZAP XR vector from Stratagene and packaged using Gigapack III Gold packaging extracts. Plasmids containing cDNA inserts were excised from the recombinant lambda ZAP phage using Ex-Assist helper phage and propagated in XLOLR cells."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          498 GIIGGIGAGCITAICGCGGCCGGCCGGIGAIIGIGAIIGCAGCIICIIIIACIAAIGIT 557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              236 aacgteettagateacaegttettgaagteaceteeggtteggaeatateegaggeagte 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         324 ACAAATGICAGTATCCGGCAACCAG-----CGGCGGCTGGTGGTGTTTACGCTACAT 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         176 cgtcctgcaggttccaaaaacaaacccaaacctccgacgattataactagagatagtcct 235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  116 ggtggagccaccagctcagccacagcctctggctcttcctccggacgtcgtccacgtggt 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       84 GGTTTAGAGCTTGGTTCAGCAGCCGGACCAGGAGATGTGGTAGGCCGCCGTCCACGCGGC 143
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                                                                                                                                                                                                                                                                                                                                                          Score 208.6; DB 10; Length 759; Pred. No. 1.1e-46;
                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches 174; Indels
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AW585780
/lab_host="E. coli strain XLOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         596 gittatgataggitaccgaitgaagagga 624
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64.68;
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/lab_host="E. coll strain XLOLR"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2: Ahol: cDNA was prepared from poly4+ enriched RNA from roots harvested at 10, 17, 22, 31 and 38 days post-incollation with Glomus versiforme. The cDNA was directionally ligated into the Unizap XR vector from directionally ligated into the Unizap XR vector from the Unizap XR vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Medicago truncatula/Glomus versiforme mixed EST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="roots colonized with Glomus versiforme"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /cultivar="Medicago truncatula genotype A17"
/db xref="taxon:119092"
/clone="pMHAM-39B13"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21.1%; Score 206; DB 9; Length 597; 66.7%; Pred. No. 5.1e-46; ive 0; Mismatches 150; Indels
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Tel: 580-223-5810
                                                                                                                                                                                                                                          TIGR sequence name:MTDAG07TK
More information is available at.
'http://chrysie.tamu.edu/medicago'
Seq primer: SKmod (CTA gAA CTA gtg gAT CC).
Plant Biology Division
The Samuel Roberts Noble Foundation
                                                                                                                                                                                       Email: mjharrisonenoble.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="MHAM"
                                                                                                                                                                                                                              Noble EST name: N254708e
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                                                                                                                                                        Fax: 580-221-7380
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BH550632
BH550632.1 GI:17802412
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//dev_stage="effective root nodules harvested one month
post incoulation with Sinchitzoblum melilot;
//dab_nost="E. col; strain XLOIR"
//note="Vector: pBluescript SK-; Site_1: EcoR; Site_2:
Xhoi; cDNA was prepared from polyA+ enriched RNA from
effective root nodules harvested one month post
incoulation with Sincrhizoblum meliloti. The cDNA was
stratagene and porchizoblum meliloti. The cDNA was
stratagene and postaged using Gloapack III Gold packaging
extracts. Plasmids containing cDNA inserts were excised
from the recombinant lambda-ZAP phage using Ex-Assist
helper phage and propagated in XLOIR cells."
                                         BG583651
EST485403 GVN Medicago truncatula cDNA clone pGVN-74E21 5' end,
                                                                                                                                                                                                                                                                                                       Fedorova, M., Pierson, B.L., Samac, D.A., Vance, C.P., Gantt, G.S., Town, C.D., Van Aken, S., Utterback, T., Cho, J. and Fraser, C.M. ESTs from one month old nitrogen-fixing root nodules of Medicago truncatula, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: vance004@maroon.tc.umn.edu
University of Minnesota name: M384729e TIGR sequence name:
MTCEM35TK More information is available at: http://www.medicago.org
Seq primer: SKmod (CTA gAA CTA gtg gAT CC).
Location/Qualifiers
                                                                                                                                                                                 Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
                                                                                                                                                                                                                                                                                                                                                                                                                                Department of Agronow and Plant Genetics
University of Minnesota
411 Borlaug Hall, 1991 Upper Buford Circle, St.Paul, MN 55108 USA
Tel: 612 625 5715
Fax: 651-649-5058
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           186 AACACTCTCAGAGCTCATATTCTTGAAGTTGCCGGCGGTTCAGATGTTTTTGAATGCGTA 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tccacctacgccactcgtcgcggcgtgcgtttgcattataagcggcacgggtgcggtc 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Medicago truncatula"
/cultivar="genotype A17"
/db_xref="taxon:3880"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone-"pGVN-74E21"
                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Carroll P. Vance
                                                                                                                      BG583651.1 GI:13598715
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                                                                                 mRNA sequence.
BG583651
                                                                                                                                                                  barrel medic.
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GSS 14-DEC-2001
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
                                                                                                                                 246 TCTACCTATGCTCGCCGCCGTCAACGTGGGATCTGTGTTCTCAGCGGCAGTGGCACTGTG 305
                                            356 actaacgtcacgatacggcaacctgcggctcggctggtggaggtgtgattaccctgcat 415
                                                                           476 gcaggaggtttgacggtgtatctagccggaggtcaaggacaagttgtaggaggga-atgt 534
                                                                                                                                                                                                                                                     535 ggctggttcgttaattgcttcgggaccggtagtgttgatggctgcttctttgcaaacgc 594
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: 301-838-3523
Fax: 301-838-3529
Email: cdcown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Sq primer: TR
Class: sheared ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 876)
Town,C.D., Van Aken,S., Utterback,T. and Fraser,C.M. Whole genome shotgun sequencing of Brassica oleracea Unpublished (2001)
Other_GSSS: BOGUC18TF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9712 Medical Center Drive, Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA
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                                                                                                                                                                                                                                                                                                                                                                                                     595 agtttatgataggttaccgattgaagaga 624
                                                                                                                                                                                                                                                                                                                                                                                                                                                  541 TGCTTATGAGAAATTGCCGTTGGAAGAGGA 570
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/clone="BOGUC18"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AW774484 688 bp mRNA linear EST 07-SEP-2000 EST3333635 KV3 Medicago truncatula cDNA clone pKV3-22P11, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           from roots of Medicago truncatula after Rhizobium inoculation
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VandenBosch, K., Hurt, J., Moore, J., Beremand, P., Peng, H., Ellis, L.,
Town, C.D., Bowman, C.L., Craven, M.B., Hansen, T.S., Holt, I.E. and
Fraser, C.M.
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/dev_stage="3 days post-inoculation with Sinorhizobium
meliloti"
                                                                                                                                                                                                                                                                                                                                                                                         511 TGACGACTCATGGGAACAATGGTGGAACTGAAGCCGGAGCTGGAGGGATTGTGACTTTAC 452
                                                                                                                                                                                                                                                 414 atggtcggtttgacattttgtctttgaccggtactgcgcttccaccgcctgcaccaccgg 473
                                                                                                                                                                                                                                                                       gagcaggaggtttgacggtgtatctagccggaggtcaaggacaagttgtaggagggaatg 533
                                                                                                                                                                                                                                                                                                                                                        391 GAIGCGGIGGILIATCIAICTITGIIGCIGGIGAACAAGGICGGAIGAICGGAGGAGAG 332
                                                        261 aagtcaceteeggtteggacatateegaggeagteteeacetaegeeactegtegegget 320
                                                                                                                                                                             -----tggaggtgtgattaccctgc 413
691 CGAAGCCACCGGTGATTGTGACAAGAGATAGCCCCAACGTGCTTAGATCTCATGTTCTTG 632
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http://chrysie.tamu.edu/medicago
seq primer: SKmod (CTA gAA CTA gtg gAT CC).
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  594 cagittaigataggitaccgailgaagaggaagaa 628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      271 CAACTTTGAAAGGCTTCCGCTTGAAGATGAAGGA 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 College Station, TX 77843-3258, USA Tel: 409 845 7707
Fax: 409 845 2891
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/db_xref="taxon:3880"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: kate@mail.bio.tamu.edu
Texas A&M EST name:T257903e
TIGR sequence name:MTEBA90TK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="pKV3-22P11"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1999)
Contact: VandenBosch K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AW774484.1 GI:7718401
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                                                                                                                                                                                       381 cggctccggctgg-----
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AW774484
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JOURNAL
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Fedorova, Pierson, B.L., Samac, D.A., Vance, C.P., Gantt, J.S., Peng, H., Ellis, L., Town, C.D., Bowman, C.L., Craven, M.B., Hansen, T.S., Holt, I.E. and Fraser, C.M.
ESTS from one month old nitrogen-fixing root nodules of Medicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EST316591 GVN Medicago truncatula cDNA clone pGVN-50F8, mRNA
       Anote—"Vector: pBluescript SK -: Site_1: EcoNI; Site_2:
XhoI: cDNA was prepared from polyA+ enriched RNA. The cDNA
was directionally ligated into the Unizap XR vector from
Stratagene and packaged using Gigapack III Gold packaging
strates. Plasmids containing cDNA inserts were excised
from the recombinant lambda-Zap phage using Ex-assist
helper phage and propagated in XLOLR cells."
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
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                                                                                                                                                                                                                                                                                                                             Gaps
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9
                                                                                                                                                                                                                                                                    tch 19.8%; Score 192.4; DB 9; Length 688; al Similarity 64.2%; Pred. No. 3.1e-42; 308; Conservative 0; Mismatches 166; Indels 6;
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/lab_host="E. coli strain XLOLR"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AW574000.1 GI:7238733
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Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papillonoldeae; Trifolleae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI; cDNA was prepared from polyA+ enriched RNA. The cDNA was directionally ligated into the Unizap XR vector from Stratagene and packaged using Gigapack III Gold packaging extracts. Plasmids containing cDNA inserts were exclaed from the recombinant lambda-Zap phage using Ex-assist from the rad propagated in SOLR cells. " I sasist 161 c 191 g 2.21 t
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/dev_stage="24 hours after treatment in the dark at 26 C with 0.5 mg/ml oligogalacturonides (DP 6-20) in the presence of 100 ug/ml Gentamicin"
/lab_host="XLOLR"
                  EST508763 HOGA Medicago truncatula cDNA clone pHOGA-15F24 5' end
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Hahn, M.G., Ojanen-Reuhs, T., Samac, D., Town, C.D., Van Aken, S., Utterback, T., Cho, J. and Fraser, C.M.
ESTS from roots of Medicago truncatula treated with Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                218 ataactagagatagtectaaegteettagateaegettettgaagteaeeteeggtteg 277
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      G390750e TIGR sequence name: MTMBV36TK More information is available at: www.medicago.org
Seq primer: SKmod (CTA gAA CTA gtg gAT CC).
Location/Qualifiers
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Best Local Similarity 64.2%; Pred. No. 3.3e-42;
Matches 308; Conservative 0; Mismatches 166; Indels
                                                                                                                                                                                                                                                                                                                                                                                Contact: Michael G. Hahn
Complex Carbohydrate Research Center
University of Georgia
220 Riverbend Road, Athens, GA 30602-4712, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Medicago truncatula"
/cultivar="A17"
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/clone="pHOGA-15F24"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hahn@ccrc.uga.edu
                                                                                BG647144.1 GI:13782256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tel: 706-542-4457
Fax: 706-542-4412
                                         mRNA sequence.
BG647144
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                  DEFINITION
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                                                           ACCESSION
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SOURCE
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post incoulation with SinchHzobium meliloti"
/lab_host="E. coll strain XLOLR"
/lab_host="E. coll strain XLOLR"
/note="Vector: pBluescript SK-; Site_1: EcoR; Site_2:
XhoI: cDNA was prepared from polyA+ enriched RNA from
effective root nodules harvested one month post
incoulation with Sinchizobium meliloti. The cDNA was
directionally ligated into the Uni-ZAP XR vector from
extracts. plasmids containing cDNA inserts were excised
from the recombinant lambda-ZAP phage using Ex-Assist
helper phage and propagated in XLOLR cells."

76 a 146 c 182 g 185 t lothers
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411 Borlaug Hall, 1991 Upper Buford Circle, St.Paul, MN 55108 USA
Tel: 612 625 5718
Fax: 651-649-6058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 136 GGTCGCAGGCGAGGGGAAGACCTCCGGGCTCAAAGAACAAACCTAAACCACGGTGATC 195
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                                                         Email: vance004@maroon.tc.umn.edu
Minnesota EST name:M228988
More information is available at.
'http://chrysie.tamu.edu/medicago'
Seq primer: SKmod (CTR AAA GTA 9tg GAT CC).
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/db_xref="taxon:3880"
/clone="pGVN-50F8"
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/tissue_type="roots colonized with Glomus versiforme"
/dev_stage="Roots harvested at 10, 17, 22, 31 and 38 days
post-inoculation with Glomus versiforme. The library was
made from a mixture of RNA from each of these stages."
/lab_most="E. coli strain XLOLR"
/lab_most="E. coli strain XLOLR"
/lote="Vector: pBluescript SR.' site_1: ECORT; Site_2:
/note="Vector: pBluescript SR.' site_1: ECORT; Site_2:
XhOI; cDNA was prepared from polyA+ enriched RNA from
roots harvested at 10, 17, 22, 31 and 38 days
post-inoculation with Glomus versiforme. The cDNA was
piectionally ligated into the Unizap XR vector from
directionally ligated into the Unizap XR vector from
stratagene and packaged using Gigapack III Gold packaging
extracts. Plasmids containing cDNA inserts were excised
from the recombinant lambda-Zap phage using Ex-assist
helper phage and propagated in XLOLR cells."

74 a 140 c 182 g 175 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Medicago truncatula/Glomus versiforme mixed EST library.
Medicago truncatula/Glomus versiforme mixed EST library
Eukaryota; mixed EST libraries.
1 (bases 1 to 671)
Harrison, M.J., Liu, J., Town, C.D., Van Aken, S., Utterback, T., Cho, J.
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                                                                                                                                                                                                                                                                                                                              linear EST 11-APR-2001
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                                                                                                                                                                          Noble EST name: N386601e TiGR sequence name: MTDDH38TK More information is available at: http://www.medicago.org seq primer: SKmod (CTA gAA CTA gtg gAT CC).
Location/Qualifiers
                                                                                     518 gttgtaggagggaatgtggctggttcgttaattgcttcgggaccggtagtgttgatggct
                                                                                                                              610 GTTGTGGGAGGAAATGTTGTTGGTCCTTTGGTTGCTTCTGGACCGGTTATTGTCATCGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /cultivar="Medicago truncatula genotype A17"
/db_xref="taxon:119092"
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The Samuel Roberts Noble Foundation
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/clone_lib="MHAM"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Glomus versiforme, 2001
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                          BG587531.1 GI:13602595
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Best Local Similarity 64.09
Matches 307; Conservative
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EST 05-SEP-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VandenBosch,K., Endre,G., Hur,J., Moore,J., Beremand,P., Ellis,L.,
Town,C.D., Bowman,C.L., Craven,M.B., Hansen,T.S., Holt,I.E. and
Fraser,C.M.
                                                                                                                                                                                                                                                                                                                                      518 gitgiaggaggaaigiggciggitcgitaaiigcitcgggaccggiagigitgaiggci 577
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                                                                                                                                                                                                                                                     122 AGTGGGAGTGGAACACTCACTAACGTGACCTTGCGACAGCCAG-----CTGCCGCAGGA 375
                                                                                                                                                                                                                                                                                                                398 ggtgtgattaccctgcatggtcggtttgacattttgtctttgaccggtactgcgcttcca 457
278 gacatatccgaggcagtctccacctacgccactcgtcgcggctgcggcgtttgcattata 337
                                                                                                                                                              262 GATGTGTTTGACTCTGTGGCTACTTATGCAAGAAGAGGGCTCAAGAGGGATCTGTGTCCTT 321
                                                                                                                                                                                                                           338 agcggcacgggtgcggtcactaacgtcacgatacggcaacctgcggctccggctggtgga 397
                                                                                     BE203784 11near EST 05-SE EST396460 KVO Medicago truncatula CDNA clone pKVO-11B13, mRNA
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/dev_stage="Immediately prior to inoculation with
Sinorhizoblum meliloti (0 hour)"
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Seq primer: SKmod (CTA gAA CTA gtg gAT CC).
Location/Qualifiers
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/cultivar="genotype A17"
/db_xref="taxon:3880"
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Tel: 409 845 7707
Fax: 409 845 2891
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TIGR sequence name:MTGAG07TK
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/clone_lib="KV0"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1999)
Contact: VandenBosch K
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EST467343 tomato crown gall Lycopersicon esculentum cDNA clone acrobibili 5' sequence, mRNA sequence.
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van der Hoeven,R., Sun,H., Cho,J., Utterback,T., Hansen,C., Ronning
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons; core eudicots;
Asteridae, euasterida I; Solanales; Solanaceae; Solanum;
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/strain="TO1000bH3"
/db_xref="taxon:3712"
/db_cref="taxon:3712"
/clone="BOGGXK9"
/clone=lib="BOGK"
/note="Vector: pHOS1; Site_1: BstXI; 2-3 kb sheared
/note="Vector: pHOS1; Site_1: BstXI; 2-3 kb sheared
/note="taxon"
/note="
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               h Similarity 62.2%; Pred. No. 6.9e-39; Length 782; Similarity 62.2%; Pred. No. 6.9e-39; 17; Conservative 0; Mismatches 166; Indels 27;
DNA is from a doubled haploid provided by Tom Osborn.
Seg primer: TF
Class: sheared ends.
Location/Qualifiers
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BG134451
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/lab_host="E.col1 strain XLOLR"
//note="Vector: pBluescript SK -; Site_1: EcoRI; Site_2:
//note="Vector: pBluescript SK -; Site_1: EcoRI; Site_2:
//note may a prepared from polya+ enriched RNN. The cDNA
was directionally ligated into the Unizap XR vector from
Stratagene and packaged using Gigapack III Gold packaging
extracts. Plasmids containing cDNA inserts were excised
from the recombinant lambda-Zap phage using Ex-assist
helper phage and propagated in XLOLR cells."
                                                                                                                                                                                                                                                                                                                                                                                                                       ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BH419879 782 bp DNA linear GSS 12-DEC-2001
BOGGX69TF BOGG Brassica oleracea genomic clone BOGGX69, DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 GATGGAAGTTGCAGACGGTTGTGACGTTGTTGAAAGTGTCAACAACTTCGCTAGACGCCG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      375
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                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 256 tettgaagteaceteeggtteggacatateegaggeagteteeacetaegeeactegteg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cggctgcggcgtttgcattataagcggcacgggtgcggtcactaacgtcacgatacggca
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9
                                                                                                                                                                                                                                                                                                                                                            Length 449;
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Town,C.D., Van Aken,S., Utterback,T. and Fraser,C.M. Whole genome shotgen sequencing of Brassica oleracea Other_GSSs: BOGGX69TR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9712 Medical Center Drive, Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                         Query Match 19.3%; Score 187.6; DB 9; Best Local Similarity 66.4%; Pred. No. 5.7e-41; Matches 287; Conservative 0; Mismatches 139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BH419879.1 GI:17605607
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Fax: 301-838-0208
Email: cdtown@tigr.org
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LOCUS
DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 CGTCAACAATTACGCTCGCCGAAGAGGGGAGGTGTCTCCATTCTCAGTGGTAACGGCGC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ggtcactaacgtcacgatacggcaacctgcggctccggctgg------ 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 GGTGGCTAACCTCACTCTCCGACAGCGGGTGACGACTCATGGGAACAATGGTGGAACTGA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----tggaggtgtgattaccctgcatggtcggtttgacattttgtctttgaccgg 444
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                232 tectaaegteettagateaeaegttettgaagteaeeteeggtteggaeatateegagge 291
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    565 agtgttgatggctgcttcttttgcaaacgcagtttatgataggttaccgattgaagagga 624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GATACTGATGGCTGCATCGTTCTCCAACGCAACTTTTGAAAGGCTTCCGCTTGAAGATGA 480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="BoGy"
/note="Vector: pHOS1; Site_l: BstXI; 2-3 kb sheared
genomic DNA inserted into pHOS1 using BstXI linkers"
161 c 215 g 208 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             292 agtctccacctacgccactcgtcgcggctgcggcgtttgcattataagcggcacgggtgc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 178.4; DB 12; Length 765;
Pred. No. 2.5e-38;
0; Mismatches 151; Indels 27;
                                                                                                                                                                                                                                                                                                                   9712 Medical Center Drive, Rockville, MD 20850, USA. Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn. Seq primer: TR
                                                                                                                                                                                             Town, C.D., Van Aken, S., Utterback, T. and Fraser, C.M. Whole genome shotgun sequencing of Brassica oleracea Unpublished (2001)
Other_GSSs: BOGXI73TF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1. .765
/organism="Brassica oleracea"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /strain="TO1000DH3"
/db_xref="taxon:3712"
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="BOGYI73
                                       GI:17690087
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63.2%;
                                                                                                                                                                                                                                                                                Contact: Chris Town
                                                                                 Brassica oleracea.
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                                                                                                   Brassica oleracea
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ви481983.1
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                                                                                                                                                                                                                                                                                                                                                                           /note="Vector: pBluescript SK(-); Site_1: EcoR1; Site_2: Xhol; Four wk old greenhouse plants were stab inoculated on stem with Agrobacterium tumefaciens C58 (Dr. T.J. Burr, Cornell U.). Galls were allowed to develop for another 4 wks, when gall tissue was frozen in liquid nitrogen."
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pOGYI73TR BOGY Brassica oleracea genomic clone BOGYI73, DNA
                                                                                                                                                                                                                                  /db_rref="taxx0:4081"
/db_rref="TOE16116"
/clone="toTOE16116"
/clone_ib="come crown gall"
/tissue_type="crown gall"
/dev_stage="crown galls from full-grown plants (8 wks old
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ccggctggtggaggtgtgattaccctgcatggtcggtttgacattttgtctttgaccggt 445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cotocgacgattataactagagatagtcctaacgtccttagatcacacgttcttgaagtc 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   266 acctccggttcggacatatccgaggcagtctccacctacgccactcgtcgcggctgcggc 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gtttgcattataagcggcacgggtgcggtcactaacgtcacgatacggcaacctgcggct 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   217 GTTTGTATTCTTAGTGGTAGCGCACAGTTACCAACGTCAACCTTCGTCAGCCTGC---- 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               125 ACGGTGCTTCCTCCGCCTGCACCGCCTCCAGTGGGATCTCTATATTTTTATCAGGT 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              273 ------TGCAAGTGTAGTCACACTCCACGGACGTTTCGAAATACTTAGCCTCTCAGGT 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              385 GGACAAGGACAAGTGGTTGGAGGATCCGTTGTAGGGCCTTTGATCGCATCAGGTCCAGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gtgttgatggctgcttcttttgcaaacgcagtttatgataggttaccgattgaagaggaa 625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           157 TCGACCGATGTTGATATCATGGAAAGTATCTCCAATTACGCAAGGCGGAGAGGGAGAGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ggtcaaggacaagttgtaggaagggaatgtggctggttcgttaattgcttcgggaccggta
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12;
                                                                        Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 10; Length 534;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                      tomato crown gall tissue
                                                                                                                                                                                                 /organism="Lycopersicon esculentum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 179.2; DB 10;
Pred. No. 1.3e-38;
0; Mismatches 168;
                                                                                                                                                                                                                    /cultivar="TĀ496
                                                                                                                                                                                                                                                                                                                                                           /lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
,C. and Tanksley,S.
Generation of ESTs from
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18.4%;
62.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                          1, .534
                                                            Contact: CUGI
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ORIGIN
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                                       JOURNAL
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                                                                                                                                                              FEATURES
                  TITLE
                                                            COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                    RESULT 1
AW776082
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                                                                                                                                                                                                                                                          Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                            (bases 1 to 488)
Journet, E. P., Crespeau, H., van-Tuinen, D., Gouzy, J., Jaillon, O.,
Journet, E. P., Carreau, V., Chatagnier, O., Kahn, D., Gianinazzi-Pearson
, V. and Gamas, P.
Medicago truncatula ESTs from nitrogen-starved roots
                                                                                                                                                                                                                                                                                                                                                                                                                                            Genoscope - Centre National de Sequencage
pp 191 91006 EVRY cedex - France
Email: seqrefégenoscope.cns.fr
Contact : Pascal Gamas and Etienne-Pascal Journet, Laboratoire de
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Blologie Moleculaire des Relations Plantes-Microorganismes, CNRS-INRA, BP 27 31326 Castanet-Tolosan Cedex, France (Email: Mt-est@toulouse.inra.fr Website: http://sequence.toulouse.inra.fr/Mtruncatula.html).
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               189 ccaaaaacaaacccaaacctccgacgattataactagagatagtcctaacgtccttagat 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         249 cacacgiticitigaagicacciccggiticggacataticcgaggcagiciticcacctacgcca 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98 CCCACGTGATGGAAGTTGCAAATGGATGTGACATCATGGAAAGTGTGACGGTCTTTGCGC 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  309 ctcgtcgcggctgcggcgtttgcattataagcggcacgggtgcggtcactaacgtcacga 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   158 GAAGGAGGCAGCGTGGTCTTGCATAGCGGAAGTGGGACCGTCACAAACGTGACTC 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18 CGAAAACAAACCACCTATCATCATCACGAGGACAGCGCGAACGCCACTCCGAT 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ..
9
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                                                                                                                                                                AL366947.1 GI:9666700
                                                                                                                                                                                                                        Medicago truncatula
                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Genoscope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 64.1
Matches 286; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (2000)
                                                                                                                                                                                                    barrel medic.
                                                                                                                             sequence.
                                                                                                                                                                                                                                                                                                 Medicago.
481 AGGA 484
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                                                                                                          DEFINITION
                                                                                                                                                                                                                        ORGANISM
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JOURNAL
COMMENT
                                                      RESULT 13
                                                                                                                                              ACCESSION
                                                                                                                                                                                                                                                                                                                  REFERENCE
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KEYWORDS
SOURCE
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Colletotrichum trifolii
Unpublished (2000)
Contact: Deborah A. Samac
Department of Plant Pathology
University of Minnesota
495 Borlaug Hall, 1991 Upper Buford Circle, St. Paul, MN 55108, USA
Pax: 651 649 5058
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Fedorova, M., Pierson, B.L., Samac, D.A., Vance, C.P., Gantt, G.S., Peng Fedorova, M., Person, B.L., Bowman, C.L., Craven, M.B., Hansen, T.S., H., Ellis, L., Town, C.D., Bowman, C.L., Craven, M.B., Hansen, T.S., Holt, I.E. and Fraser, C.M.
ESTS from leaves of Medicago truncatula after inoculation with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AW776082 582 bp mRNA linear EST 07-SEP-2000 EST335147 DSIL Medicago truncatula cDNA clone pbSIL-6E7, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papillonoideae; Trifolleae;
                                                                                                                                                                                                           489 cggtgtatctagccggaggtcaaggacaagttgtaggagggaatgtggctggttcgttaa 548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          549 ttgcttcgggaccggtagtgttgatggctgcttcttttgcaaacgcagtttatgataggt 608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          218 TCCGTCAACCAGCATCGCC----TGGTGCGGTAGTCACACTTCATGGAAGATTTGAGA 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 332 CCATATATCTAGCTGGTGGACAAGGACAGGTCGTCGGTGGTAGCGTGGGGGCCGTTGT 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="leaves infected with Colletotrichum trifolil"
369 tacggcaacctgcggctccggctggaggtgtgattaccctgcatggtcggtttgaca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seq primer: SKmod (CTA gAA CTA gtg gAT CC).
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: debbys@puccini.crl.umn.edu
Minnesota sequence name:M259415e
TIGR sequence name:WFAM28TK
More information is available at.
http://chrysie.tamu.edu/medicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /cultivar="genotype A17"
/db_xref="taxon:3880"
/clone="pDSIL-6E7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   609 taccgattgaagaggaagaaacccca 634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="DSIL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AW776082.1 GI:7765895
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source

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1;
                  from the recombinant lambda-ZAP phage using Ex-Assist helper phage and propagated in XLOLR cells. Note: EST may be of fungal origin." 129 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GSS 14-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
extracts. Plasmids containing cDNA inserts were excised
                                                                                                                                                                                                                                                                                                                356 actaacgtcacgatacggcaacctgcggctccggctggtggaggtgtgattaccctgcat 415
                                                                                                                                                                                                                                         116 ggtggagccaccagctcagccacagcctctggctcttcctccggacgtcgtccacgtggt 175
                                                                                                                                                                                                                                                                    236 aacgteettagateacaegttettgaagteaceteeggtteggaeatateegaggeagte 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tocacetacgecactegtegeggetgeggegtttgeattataageggeaegggtgeggte 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           324 TCTACCTATGCTCGCCGCCGCCGTCAACGTGTTCTCAGCGGCAGTGGCACTGTG 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99tc99ttt9acattttgtctttgaccggtactgcgcttccaccgcctgcaccacggga 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         438 GGAAGATITGAGATATTATCCTTGTCTGGATCTTTTCTGCCACCACCACCTCCTCCCGGA 497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     476 gcaggaggtttgacggtgtatctagccggaggtcaaggacaagttgtaggagggaatgtg 535
                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             498 GCAACTAGCTTAACGATTTATCTTGCTGGAGGACAAGGACAAGTGGTGGGGGAGGTAGCGTG 557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BOHCV23TR BOHC Brassica oleracea genomic clone BOHCV23, DNA
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9
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Seg primer: TR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Town, C.D., Van Aken, S., Utterback, T. and Fraser, C.M. Whole genome shotgun sequencing of Brassica oleracea Ombublished (2001)
Other GSSS: BOHCV3TFF
Contact: Chris Town
                                                                                                                                                             Length 582;
                                                                                                                                                       Query Match 17.9%; Score 174; DB 9; Length 58 Best Local Similarity 63.6%; Pred. No. 3.7e-37; Matches 283; Conservative 0; Mismatches 156; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9712 Medical Center Drive, Rockville, MD 20850,
Tel: 301-838-3523
Fax: 301-838-0208
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/organism="Brassica oleracea"
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ATF23E12 86710 bp DNA 11near CHANGOLARBE-19999 Arabidopsis thaliana DNA chromosome 4, BAC clone F23E12 (ESSA
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosida II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 86710)
Bevan,M., Hilbert,H., Braun,M., Holzer,E., Brandt,A.,
Duesterhoeft,A., Hoheisel,J., Mewes,H.W., Mayer,K.F.X. and
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EU Arabidopsis sequencing, project.
Direct Submission
Submitted (01-APR-1999) MIPS, at the Max-Planck-Institut fuer
Biochemie, Am Klopferspitz 18a, D-82152 Martinsried, FRG, E-mail:
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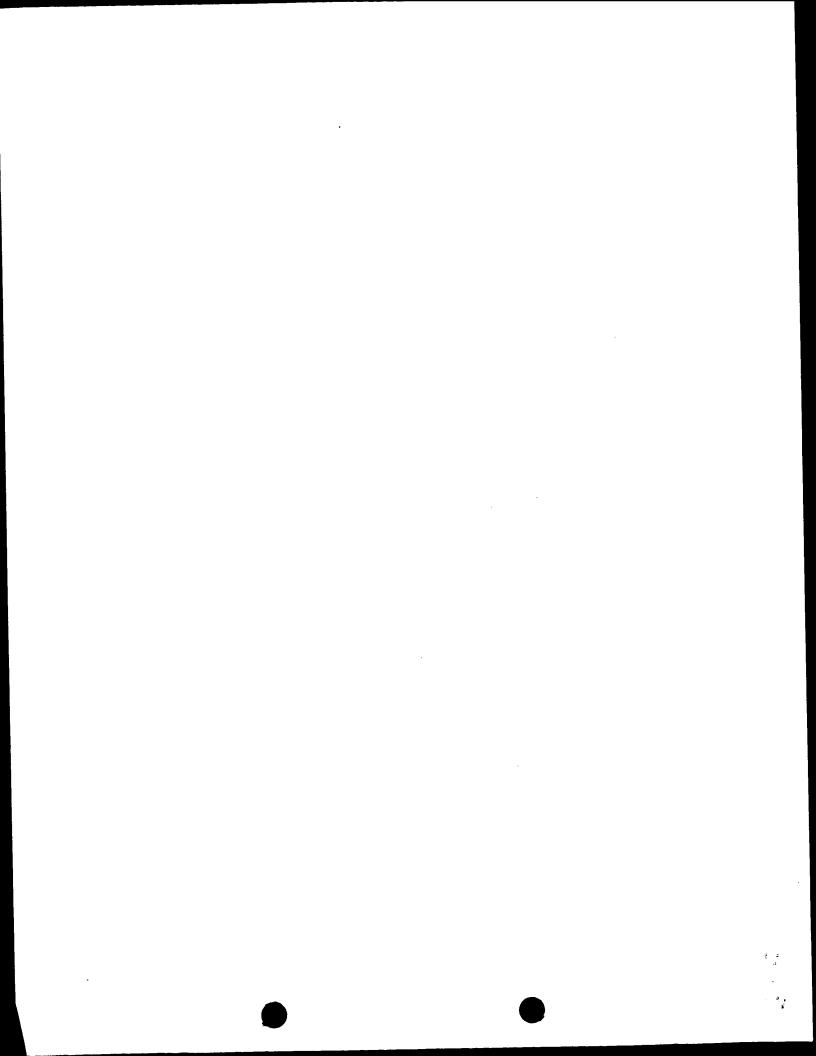
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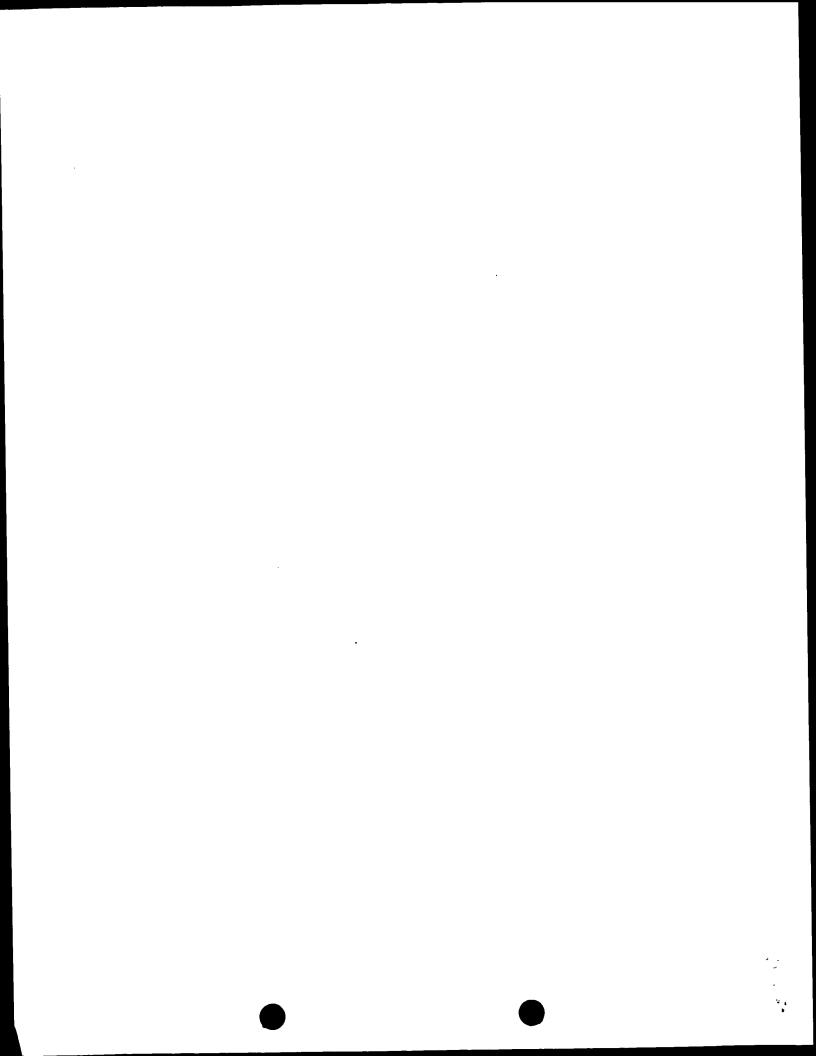
AP004319 Oryza sat AP003683 Oryza sat AC012188 Sequence AF184830 Arabidops AP003938 Oryza sat AP004680 Oryza sat



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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      schuelle@mips.blochem.mpg.de,mayer@mips.blochem.mpg.de Project Coordinator: Mike Bevan, Molecular Genetics Department, Cambridge Laboratory, John Innes Centre, Colney Lane, NR4 7UJ Norwich, UK, E-mail: michael.bevan@bbsrc.ac.uk
Information on performance of analysis and a more detailed annotation of this entry and other sequences of chromosomes 3, 4 and 5 can be viewed at: http://www.mips.blochem.mpg.de/proj/thal/.location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="SptremeL:065487"
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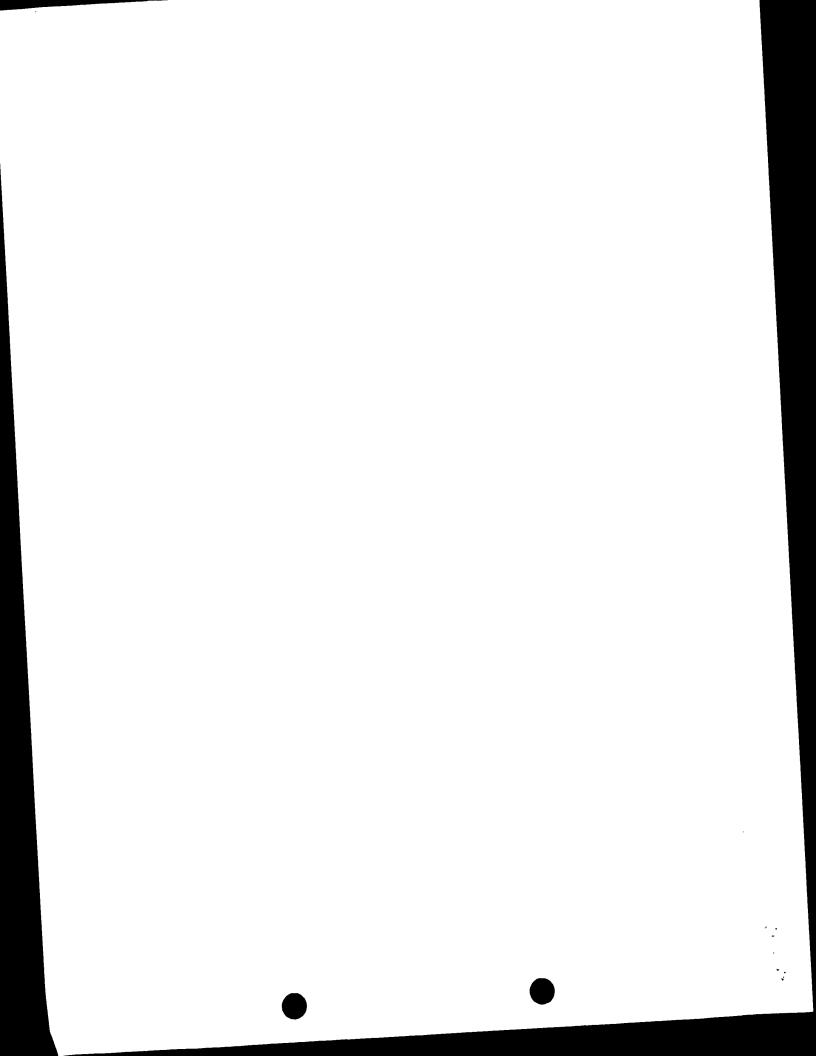


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Arabidopsis thaliana
Eukaryota: Viridiplantae; Streptophyta; Embryophyta: Tracheophyta;
Spermatophyta: Magnollophyta; eudicotyledons; core eudicots;
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[ (bases 16641 to 103350)
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Robben,J., Grymonprez,B., Volckaert,G., Mewes,H.W., Lemcke,K. and
                                                                                                                                                                                                                                                                                                                                      907 gittgogtgittgacotcaaactactaggctactagctatagcggttgogaaatgogaat 966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Jursec, summission.
Submitted (10-Mar-2000) MIPS, at the Max-Planck-Institut fuer Biochemie, Am Klopferspitz 18a, D-82152 Martinsried, FRG, E-mail: lemcke@mips.biochem.mpg.de_mayer@mips.blochem.mpg.de_mayer@mips.blochem.mpg.de_project Coordinator: Mike Bevan, Molecular Genetics Department, Cambridge Laboratory, John Innes Centre, Colney Lane, NR4 7UJ Norwich, UK, E-mail: michael.bevan@bbrc.ac.uk
Information on performance of analysis and a more detailed annotation of this entry and other sequences of chromosomes 3, 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana DNA chromosome 4, contig fragment No. 83.
                                                                                                                                                                                                                                      Hilbert, H., Braun, M., Holzer, E., Brandt, A., Duesterhoeft, A., Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 (Dasses 120761 to 197859)
Rose, M., Hempel, S., Entlan, K.-D., Mewes, H.W., Lemcke, K. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 (bases I to 24256)
Murphy, G., Ridley, P., Hudson, S., Mewes, H.W., Lemcke, K. and
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EU Arabidopsis sequencing, project.
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                              OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Perfect score:
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al number of hits satisfying chosen parameters: Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries _mum DB seq length: 0
Maximum DB seq length: 2000000000

562222

SPTREMBL_19:* Database :

sp_arches:*
sp_bacteria:*
sp_fung1:*
sp_fung1:*
sp_human:*
sp_nammal:*
sp_nammal:*
sp_organelle:*
sp_phage:*
sp_phage:*
sp_plant:*
sp_rodent:*
sp_rodent:*
sp_vtrus:* sp_unclassified:* sp_rvirus:*
sp_bacteriap:*
sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

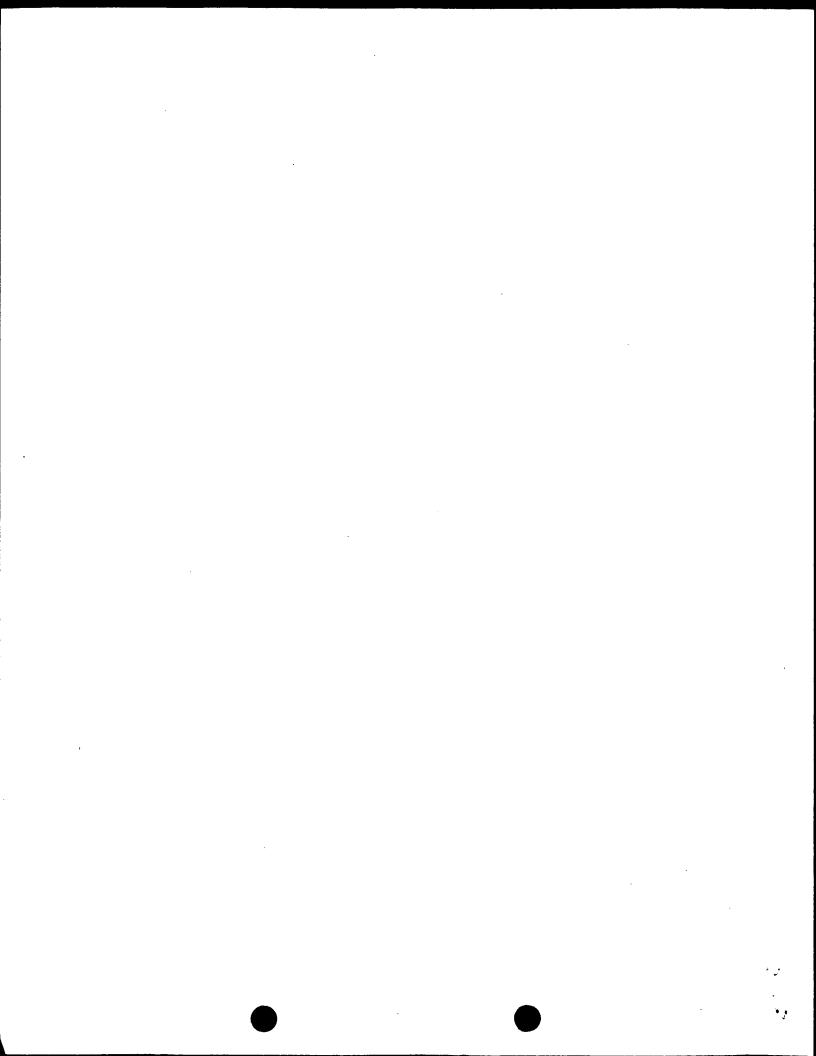
098769 arabidopsis 02362 arabidopsis 020877 arabidopsis 020130 arabidopsis 022130 arabidopsis 098270 arabidopsis 049662 arabidopsis 0912x7 arabidopsis 0912x7 arabidopsis 0912x2 arabidopsis 0912x2 arabidopsis 09142 arabidopsis 09142 arabidopsis 09149 oryza sativ 065489 arabidopsis Description SUMMARIES 065489 0957C9 0957C9 0957C9 0958I7 0958I7 0957C9 0912X7 0962 0957C9 0957C9 0967C9 0967C9 0967C9 0967C9 g Query Match Length 3311 3312 3315 3315 3324 3324 3324 3265 406 404 Score Result Š. 26439

Q9xhy4 oryza sativ								049658 arabidopsis						Q9sb31 arabidopsis	_	m	_	'n	_			Q	Q23057 caenorhabd1	Q9nlp0 bos taurus	Q9gub5 galleria me	υ	O53212 mycobacter1	
Q9XHY4	Q9AYM0	Q94F52	022812	023142	Q9FHM5	Q9SH33	092RR7	049658	Q9FIR1	004696	049350	Q940I0	004695	Q9SB31	049694	098273	080834	09SR16	081321	Q9M2D3	095702	Q9V889	023057	Q9N1P0	Q9GUB5	023347	053212	092KQ8
10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10					9			9	16
771	405	351	296	351	419	826	300	334	386	347	439	439	334	404	455	365	348	418	345	348	574	848	405	818	1468	265	694	1610
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289	283	282	274	274	264.5	259	258.5	255.5	248.5	246.5	243	243	242.5	239.5	239	227	225	221	218	211.5	162.5	148	146	143.5	139	138.5	137	136.5
17	18	13	20	21												33					38	39	40	41	42	43	44	. 45

ALIGNMENTS

	ARY; PRT; 270 AA.	07, Creat	(Trembirel. 0/, Last sequence update) (Trembirel. 19, Last annotation update)	A PROTEIN.	90.	Arabidopsis thaliana (Mouse-ear cress).	Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;	Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Koslude; eurosids II: Brassicales: Brassicaceae: Arabidopsis.				E., Brandt A., Duester	Hoheisel J., Jesse T., Heijnen L., Vos P., Mewes H.W., Mayer K.F.X.,		Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.		•	Hilbert H., Braun M., Holzer E., Brandt A., Duesterhoeft A.,	., Mayer K.F.X.;	Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.			ncing project;	Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.	8730.1;	0256.1;		26774 MW; 4C21487C2719E114 CRC64;	100.0%; Score 1392; DB 10; Length 270;	100.0%; Fred. No. 4./e-88; tive 0; Mismatches 0; Indels 0; Gaps
	PRELIMINARY;	(TrEMBLrel.		AL 26.8 KDA PROTEIN.	F23E12.50 OR AT4G35390.	s thaliana (Mous	Viridiplantae;	/ta; Magnollopny F: Brassicales:	-3702;		ROM N.A.	Hilbert H., Brau	., Jesse T., Hei		(APR-1998) to th		ROM N.A.	, Braun M., Holz	, Lemcke K., May	(MAR-2000) to th		ROM N.A.	EU Arabidopsis sequencing project;	(MAR-2000) to th	2604; CAA18730.1	EMBL; AL161587; CAB80256.1;	al protein.	SEQUENCE 270 AA; 26774		ğ
RESULT 1 065489	065489		01-A0G-1998 01-DEC-2001																										Query Match	Best Local Similarity Matches 270; Conserv
RE 06	E S	E E	<u> </u>	DE	B	os	8	88	ő	RN	RP	RA	RA	RA	RL	RN	RP	RA	RA	RL	RN	RP	RA	RL	DR	DR	K	S		

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                                                                                                                                                                      61 LKSHVLEVTSGSDISEAVSTYATRRGCGVCIISGTGAVTNVTIRQPAAPAGGGVITLHGR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                 61 LRSHVLEVTSGSDISEAVSTYATRRGCGVCIISGTGAVTNVTIRQPAAPAGGGVITLHGR 120
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                                                                9
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                                                                                                                                                                                                                                                                                                                                                                                                                DRLP I EEEET PPPRTTGVQQQPEASQSSEVTGSGAQACESNLQGGNGGGGVAFYNLGMN
                                    1 MELNRSEADEAKAETTPTGGATSSATASGSSSGRRPRGRPAGSKNKPKPPTIITRDSPNV
MELNRSEADEAKAETTPTGGATSSATASGSSSGRRPRGRPAGSKNKPKPPT11TRDSPNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN-CV. COLUMBIA;
Federspiel N.A., Palm C.J., Conway A.B., Conn L., Hansen N.F.,
Altafi H., Araujo R., Huizar L., Rowley D., Buehler E., Dunn P.,
Gonzalez A., Kremenetskata I., Kim C., Lenz C., Li J., Liu S.,
Luros S., Schwartz J., Shinn P., Toriumi M., Vysotskaia V.S.,
Walker M., Yu G., Ecker J., Theologis A., Davis R.W.;
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Activation Tagging in Arabidopsis.";
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  241 MNNFQFSGGDIYGMSGGSGGGGGGTRPAF 270
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Pfam; PF02178; AT_hook; 1.
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01-MAY-2000
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MEDLINE-9812113; Pubmed-9461215;

A MEDLINE-98121113; Pubmed-9461215;

Bevan M., Bancroft I., Bent E., Love K., Goodman H., Dean C.,

Bevan M., Dancroft I., Bent E., Love K., Stlekema W., Drost L.,

Radley P., Hudson S.A., Patel K., Murphy G., Piffanelli P., Wedler H.,

Radley E., Wambutt R., Weitzenegger T., Pohl T.M., Terryn N.,

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Bentan K.D., Rieger M., Schaeffer M., Funk B., Mueller-Auer S.,

Alvey M., James R., Montfort A., Pons A., Pulydomenech P., Douka A.,

Nouchatou E., Milloni D., Hatzopoulos P., Piravandi E., Obermaler B.,

Hilbert H., Duesterhoft A., Moores T., Jones J.D.G., Eneva T.,

Palme K., Benes V., Rechman S., Ansorge W., Cooke R., Berger C.,

Delseny M., Voet M., Volckmert G., Mewes H.W., Klosterman S.,

Schueller C., Chalwatzis N.;

Analysis of 1.9 Mb of contiguous sequence from chromosome 4 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           74 ISEAVSTYATRRGCGVCIISGTGAVTNVTIRQPAAPAGGGVITLHGRFDILSLTGTALPP 133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  194 RTTGVQQQPEASQSSEVTGSGAQACESNLQGGN-----GGGGVAFYNLGMNMN-NF 244
                                                                                                                                                                                                                                                                                                                                                                                                            Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             180 YDRLPIEEEETP------PPRTTGVQQQQPEASQSSEVTGSGAQACESNLQGGNG 228
                                                                                                239 FERLPIEEEEEEGGGGGGGGGGGPPQ----MQQAPSASPPSGVTGQGQ------LGGNV 287
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       47; Indels
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Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
EMBL; 297344; CAB10560.1;
                                                                                                                                       229 GGGVAFYNLGMNMNNFQFSGGDIYGMSGGS---GGGGGGATRPAF 270
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292 Aa; 29724 MW; 2A948700FA543C4F CRC64;
                                                                                                                                                                           -----YGFSGDPHLLGWGAGTPSRPPF 311
                                                                                                                                                                                                                                                                                                                01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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                                                                                                                                                                                                                                                                              PRT;
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HYPOTHETICAL 29.7 KDA PROTEIN.
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                                                                                                                                                                                                                                                                              PRELIMINARY;
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SEQUENCE 29
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                                                                                                                                                                                             191 PP----PRTTGVQQQPEASQSSEVTGSGAQACESNLQGGNGGGGVAFYNLGMNMNNFQF 246
                                                                                                                                                         77 AVSTYATRRGCGVCIISGTGAVTNVTIRQP-----AAPAGGGVITLHGRFDILSLTGTA 130
                                                                                                                                37; Gaps
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Matches 132; Conservative
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990S-0161993.
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18-AUG-1999;
20-AUG-1999;
20-AUG-1999;
23-AUG-1999;
25-AUG-1999;
27-AUG-1999;
27-AUG-1999;
27-AUG-1999;
27-AUG-1999;
27-AUG-1999;
27-AUG-1999;
31-AUG-1999;
31-AUG-1999;
31-SEP-1999;
32-SEP-1999;
33-SEP-1999;
34-SEP-1999;
32-SEP-1999;
33-SEP-1999;
33-SEP-1999;
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39-SEP-1999;
39-SEP-1999;
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39-SEP-1999;
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22-0CT-1999;
22-0CT-1999;
25-0CT-1999;
25-0CT-1999;
26-0CT-1999;
26-0CT-1999;
26-0CT-1999;
28-0CT-1999;
28-0CT-1999;
28-0CT-1999;
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21-OCT-1999;
21-OCT-1999;
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21-OCT-1999;
21-OCT-1999;
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4-0CT-1999;
4-0CT-1999;
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
194 RTTGVQQQQPEASQSSEVTGSGAQACESNLQGGN-----GGGGVAFYNLGMNMN-NF
                                                                                                                                          Arabidopsis thaliana protein fragment SEQ ID NO: 34899.
                                                                                                AAG29344 standard; Protein; 292 AA.
                                                                                                                                                                                                                                                 990S-0123180.
990S-012548.
990S-0125648.
990S-0126264.
990S-0126785.
990S-0128244.
990S-0130047.
990S-0130449.
990S-0132484.
990S-0132484.
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99US-0134218.
99US-0134219.
                                                245 QFSGGDIYGMSGGSGGG 262
                                                             238 q1---pvegwpgnsggrg 252
                                                                                                                                                                                                                              25-FEB-2000; 2000EP-0301439
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99US-0134768.
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99US-0137724
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                                                                                                                           17-OCT-2000 (first entry)
                                                                                                                                                                                    Arabidopsis thaliana
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990S-0139899
990S-0139899
990S-0140353
990S-0140625
990S-0140823
990S-0141287
990S-0141287
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990S-0142184
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990S-0144332
990S-0144332
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990S-0144334
990S-0144333
990S-0144334
990S-0144333
990S-0144814
990S-0144333
990S-0145089
990S-0145919
990S-0147038
99US-0139456.
99US-0139457.
99US-0139458.
99US-0139460.
99US-0139461.
99US-0139463.
99US-0139463.
99US-0139463.
18-JUN-1999;
18-JUN-1999;
18-JUN-1999;
18-JUN-1999;
18-JUN-1999;
18-JUN-1999;
18-JUN-1999;
18-JUN-1999;
18-JUN-1999;
22-JUN-1999;
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12-JUL-1999;
13-JUL-1999;
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15-JUL-1999;
16-JUL-1999;
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06-AUG-1999;
06-AUG-1999;
09-AUG-1999;
09-AUG-1999;
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23-JUN-1999;
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08-JUL-1999;
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9-JUL-1999;
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02-AUG-1999
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17-AUG-1999;
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                                                                                                                                                           30-JUN-1999
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  Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                      Arabidopsis thaliana protein fragment SEQ ID NO: 34900.
  241 mnnfqfsggdiygmsggsgggggggtrpaf 270
                                                 AAG29345 standard; Protein; 254 AA
                                                                                                                                                                                                                                                                                                                   9905-0129845.
9905-0130077.
9905-0130510.
9905-0130891.
9905-0132048.
9905-0132484.
9905-0132484.
9905-0132486.
9905-0132486.
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990S-0134218.
990S-0134219.
990S-013421.
990S-013470.
990S-0134768.
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990S-0135353.
990S-0135629.
990S-0136021.
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99US-0137502.
99US-0137724.
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99US-0123180.
99US-012348.
99US-0125788.
99US-0126785.
99US-0128784.
99US-0128234.
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99US-0139492.
99US-0139454.
99US-0139455.
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99US-0138847.
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                                                                                      17-OCT-2000 (first entry)
                                                                                                                                                             Arabidopsis thaliana
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28-MAY-1999;
01-JUN-1999;
03-JUN-1999;
04-JUN-1999;
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29. MAR - 1999

10. APR - 1999

10. APR - 1999

11. APR - 1999

12. APR - 1999

23. APR - 1999

23. APR - 1999

24. MAY - 1999

10. MAY - 1999
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10-JUN-1999;
10-JUN-1999;
14-JUN-1999;
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1,8-JUN;1999;
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                                                                    AAG29345;
                               RESULT
AAG29345
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                                                                                                                    <u>ب</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Transcription factor; flowering time; transgenic plant; vernalisation; plant development; plant physiology; flowering.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LRSHVLEVTSGSDISEAVSTYATRGCGVCIISGTGAVTNVTIRQPAAPAGGGVITLHGR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 FDILSLIGTALPPPAPPGAGGLTVYLAGGQGQVVGGNVAGSLIASGPVVLMAASFANAVY 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DRLPIEEEETPPPRTTGVQQQPEASQSSEVTGSGAQACESNLQGGUGGGGVAFYNLGMN 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MELNRSEADEAKAETTPTGGATSSATASGSSSGRRPRGRPAGSKNKPKPPTIITRDSPNV 60
                                                                                                                    Samaha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acids encoding plant transcription factor polypeptides, user altering the developmental and structural characteristics of plants, e.g. corn, potato and cotton plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 1392; DB 22; Length 270; 100.0%; Pred. No. 8.6e-105; tive 0; Mismatches 0; Indels 0;
                                                                                                            Riechmann JL, Reuber L, Keddie J, Ratcliffe O, Heard J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Amino acid sequence of a plant transcription factor G1073,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241 mnnfqfsggdiygmsggsgggggatrpaf 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241 MNNFQFSGGDIYGMSGGSGGGGGGTRPAF 270
                                                                                                                                                                                                                                                                         Claim 4; Page 103-104; 140pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB67838 standard; Protein; 270 AA.
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KEDDIE J.
RATCLIFFE O.
HEARD J.
SAMAHA R.
                                                                                                                                                             WPI; 2001-335996/35
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270; Conserv
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                                                                               (JIAN/) JIANG C.
                                                                                                                                                                               N-PSDB; AAD05839
                                                                                                                              Jiang C;
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Best Local Si
Matches 270;
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 (KEDD/)
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                                HEAR/
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AAB67838
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New transgenic plant comprises a recombinant polynucleotide encoding a plant transcription factor polypeptide and has a modified flowering time or vernalization requirement.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 LRSHVLEVTSGSDISEAVSTYATRRGCGVCIISGTGAVTNVTIRQPAAPAGGGVITLHGR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 1392; DB 22; 100.0%; Pred. No. 8.6e-105;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 7; Page 94-95; 108pp; English.
                                                                                                                                                                                                                                                                                                                                                    Samaha R,
                                                                                                                                                                                                      (MEND-) MENDEL BIOTECHNOLOGY INC.
                                                                                                                             990S-0164132.
990S-0166228.
2000US-0197899.
2000US-0227439.
                                                                                     11-OCT-2000; 2000WO-US28141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the transcription factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 270; Conservative
                                                                                                                                                                                                                                                                                                                                                   ), Heard J,
Riechmann JL;
                                                                                                                                                                                                                                                                                          (JIAN/) JIANG C.
(REUB/) REUBER L.
(RIEC/) RIECHMANN J L.
Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                                             2001-266398/27.
                                                                                                                                                                                                                     RATCLIFFE O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    270 AA;
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                                                                                                                                                                                                                                                  SAMAHA R.
                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-266398/
N-PSDB; AAF80408
                                                                                                                                                                                                                                   HEARD J.
                         WO200126459-A2
                                                                                                                                                                         22-AUG-2000;
                                                                                                                              08-NOV-1999;
17-NOV-1999;
                                                                                                                                                           L7-APR-2000;
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                                                          19-APR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                 (SAMA/)
                                                                                                                                                                                                                                                                            KEDD/)
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                                                                                                                                                                                                                                   (HEAR/)
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433.882 Million cell updates/sec
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3: /SIDS5/gcgdata/geneseqy-emb1/AA1981. DAT: *
4: /SIDS5/gcgdata/geneseqy-emb1/AA1983. DAT: *
5: /SIDS5/gcgdata/geneseqy-emb1/AA1983. DAT: *
5: /SIDS5/gcgdata/geneseqy-emb1/AA1984. DAT: *
6: /SIDS5/gcgdata/geneseqy-emb1/AA1985. DAT: *
7: /SIDS5/gcgdata/geneseqy-emb1/AA1985. DAT: *
8: /SIDS5/gcgdata/geneseqy-emb1/AA1989. DAT: *
9: /SIDS5/gcgdata/geneseqy-emb1/AA1989. DAT: *
11: /SIDS5/gcgdata/geneseqy-emb1/AA1999. DAT: *
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2: /SIDS5/gcgdata/geneseqy-emb1/AA1991. DAT: *
2: /SIDS5/gcgdata/geneseqy-emb1/AA1991. DAT: *
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2: /SIDS5/gcgdata/genese
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/SIDSS/gcgdata/geneseq/geneseqp.embl/AA1994.DAT:*
/SIDSS/gcgdata/geneseq/geneseqp.embl/AA1994.DAT:*
/SIDSS/gcgdata/geneseq/geneseqp.embl/AA1996.DAT:*
/SIDSS/gcgdata/geneseq/geneseqp.embl/AA1997.DAT:*
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/SIDSS/gcgdata/geneseq/geneseqp.embl/AA1999.DAT:*
/SIDSS/gcgdata/geneseq/geneseqp.embl/AA1000.DAT:*
/SIDSS/gcgdata/geneseq/geneseqp.embl/AA2001.DAT:*
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                                                                                                                                                                                                                                                                                                         July 10, 2002, 21:20:07; Search time 69.12 Seconds
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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		ф			SUMMARIES			
Result No.	Score	Query Match	Query Match Length DB	DB	ID		Description	
7	1392	100.0	270	22	AAE01961		Arabidopsis thal	thal
7	1392	100.0	270	22	AAB67838		Amino acid seque	edne
9	646.5	46.4	254	21	AAG29345		Arabidopsis	thal
4	646.5	46.4	292	21	AAG29344	,	Arabidopsis	thal
S	637.5	45.8	280	21	AAG10650		Arabidopsis	
9	637.5	45.8	282	21	AAG10649		Arabidopsis	
7	637.5	45.8	315	21	AAG10648		Arabidopsis	
89	625.5	44.9	339	22	AAE02571		A. thaliana	
6	572	41.1	272	21	AAG21497		Arabidopsis	
10	572	41.1	272	21	AAG54092		Arabidopsis	
,11,	5,72	41.1	310	21	AAG21496		Arabidopsis	thal

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ALIGNMENTS

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Transcription factor; trait modification; structural characteristic; developmental characteristic; gene therapy; agricultural biotechnology.
                                                                              Arabidopsis thaliana transcription factor G1073.
                                                                                                                                                                 33..42
/note= "Conserved domain"
78..175
/note= "Conserved domain"
                                                                                                                                                      Location/Qualifiers
                  AAE01961 standard; Protein; 270 AA.
                                                                                                                                                                                                                                                                                                                             (MEND-) MENDEL BIOTECHNOLOGY INC.
                                                                                                                                                                                                                                                               14-NOV-2000; 2000WO-US31325
                                                                                                                                                                                                                                                                                  99US-0166228
                                                                                                                                                                                                                                                                                            17-APR-2000; 2000US-0197899
                                                                                                                                                                                                                                                                                                      22-AUG-2000; 2000US-0227439
                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                      (RIEC/) RIECHMANN J L. (REUB/) REUBER L.
                                                                                                                                   Arabidopsis thaliana.
                                                                                                                                                                                                                      WO200136444-A1.
                                                                                                                                                                                                                                                                                   17-NOV-1999;
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                                       AAE01961;
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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      78 VSTYATRRGCGVCIISGTG---AVTNVTIRQPAAP--AGGGVI-TLHGRFDILSLTGTAL 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 132 PPPAPPGAGGLTVYLAGGQQVVGGNVAGSLIASGPVVLMAASFANAVYDRLP---- 184
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Haynes S.R., Mozer B.A., Bhatia-Dey N., Dawid I.B.;
"The Drosophila fsh locus, a maternal effect homeotic gene, encodes
apparent membrane proteins.";
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191709; PR1310; PR1310; PR13709; PR13109; PR13109; PR13109; PR13109; PR13109; PR1 13, Last sequence update)
01-JAN-1990 (Rel. 13, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
Female sterile homeotic protein (Fragile-chorion membrane protein)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9.2%; Score 128.5; DB 1; Length 1150; 86.6%; Pred. No. 0.47; Ive 30; Mismatches 107; Indels 81;
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1150 AA; 109615
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Matches 79; Conservative 3
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                                                                                                                                                                                                                   13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1685 DRLKLLEAAEKEKKNOKEAAEKEQORKHHK-----SSSSSLTSAAVAQAAAIAAA 1737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1738 AAVTL-GAAAAAALASSASNPSGGSSSGG----AGSTSQQAITGDRDRDRDRERERERS 1791
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         56 DSPNVLRSHVLEVTSGSDISEAVSTYATRRGCGVCIISGTGAVTNVTIRQPAAPA---GG 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       113 GVITLHGRFDILSLTGTALPPPAPPGAGGLTVYLAGGQGQVV--------- 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   155 ------GGNVAGSLIASGPVVLMAASFANAVYDRLPIEEEETPPPRTTGVQQQPEA 205
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels 101; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7 EADEAKAETTPTGGATSSA----TASGSSSGRRPRGRPAGS----KNKPKPPTIITR 55
. Biol. 134:246-257(1989).
FUNCTION: REQUIRED MATERNALLY FOR PROPER EXPRESSION OF OTHER HOMEOTIC GENES INVOLVED IN PATTERN FORMATION, SUCH AS UBX. SIMILARITY: CONTAINS 2 BROMDOMAINS.
SIMILARITY: CONTAINS 2 BROMDOMAINS.
SIMILARITY: CONTAINS 1 ET DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 2038;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein; Bromodomain; Transmembrane; Repeat.
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-> RKPYY.
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EMBL; M23222; AAA28541.1; ALT_TERM.
EMBL; M15762; AAA70424.1; -.
EMBL; M15763; AAA70423.1; -.
EMBL; M15764; AAA70422.1; -.
PIR; A43742.
                                                                                                                                                                                                                                                                                                                                                                                                SMART; SM00297; BROWO; 2.
PROSITE; PS00633; BROMODOMAIN_1; 2.
PROSITE; PS50014; BROMODOMAIN_2; 2.
                                                                                                                                                                                                                                                                                                                     HSSP; P04002; IWFA.
FlyBase; FBGN0004656; fs(1)h.
InterPro: IPR001487; Bromodomain.
Pfam; PF00439; bromodomain; 2.
PRINTS; PR00503; BROMODOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    205332 MW;
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Best Local Similarity 23.1.,
73; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MESODERAL LAYERS.

-!- SUBCELLULAR LOADIN. Nuclear (Potential).

- ISSUE SPECIFICITY: MESODERA.

-!- DEVELOPMENTAL STACE: FIRST DETECTABLE IN THE PRESUMPTIVE MESODERA.

-!- DEVELOPMENTAL STACE: FIRST DETECTABLE IN THE PRESUMPTIVE MESODERA PRIOR TO THE SPLITTING PROCESS THAT GENERATES THE SOMATIC AND VISCERAL/ HEART HESODERA. AFFER THE SUBDIVISION. IT IS FOUND IN BOTH THE SOMATIC AND THE VISCERAL/HEART MESODERA.

-!- INDUCTION: TWI ACTIVITY IS REQUIRED FOR MEP? EXPRESSION. SNA ACTIVITY IS NEEDED FOR MAINTAINING MEP? EXPRESSION.

-!- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION
                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=94329547; PubMed=8052612;
Nguyen H.T., Bodmer R., Abmayr S.M., McDermott J.C., Spoerel N.A.;
"D-mef2: a Drosophila mesoderm-specific MADS box-containing gene with
a biphasic expression profile during embryogenesis.";
Proc. Natl. Acad. Sci. U.S.A. 91:7520-7524(1994).
- FUNCTION: TRANSCRIPTION FACTOR THAT COULD BE A KEY PLAYER IN EARLY
MESODERM DIFFERENTIATION AND MAY BE REQUIRED FOR SUBSEQUENT CELL
                                                                                                                                                                                                                                                                                                                         Lilly B., Galewsky S., Firulli A.B., Schulz R.A., Olson E.N., marger: a MADS box transcription factor expressed in differentiating mesoderm and muscle cell lineages during Drosophila embryogenesis."; Proc. Natl. Acad. Sci. U.S.A. 91:5662-5666(1994).
                                                                                                                                                                                       Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                          Drosophila melanogaster (Fruit fly).
Eukaryota, Metazoa; Arthropoda, Tracheata, Hexapoda, Insecta,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FATE SPECIFICATIONS WITHIN THE SOMATIC AND VISCERAL/HEART
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00350; MADS_BOX_1; 1.
PROSITE; PS50066; MADS_BOX_2; 1.
Transcription regulation; DNA-binding; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEF2-TYPE (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein; Differentiation; Activator.
                                                                     (Rel. 31, Created)
(Rel. 31, Last sequence update)
(Rel. 37, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POLY-SER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POLY-GLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POLY-GLY
                                  PRT;
                                                                                                                       Myocyte-specific enhancer factor 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MADS.
                                                                                                                                                                                                                                                                                                           MEDLINE-94261646; PubMed-8202544;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR002100; MADS-box.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00319; SRF-TF; 1.
PRINTS; PR00404; MADSDOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FACTORS. MEF2 SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; U03292; AAA19957.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; U07422; AAA20463.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FlyBase; FBgn0011656; Mef2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART; SM00432; MADS; 1.
                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          386
396
428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1SRS.
                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            58
380
390
421
                                                                                                                                                                                                                                  NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSSP; P11831;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Developmental
                                                                                                                                                                                                                                                                                             TISSUE=Embryo;
                                                                     01-FEB-1995
                                                                                                          15-DEC-1998
                                                                                      01-FEB-1995
                                  MEF2_DROME
P40791;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                 MEF2_DROME
RESULT
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                                                                                                                                                                                                                                                                     12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               THE REGULATION OF EUKARYOTIC GENE EXPRESSION AND AFFECT CELLULAR PROLIFERATION AND DIFFERNTIATION IN TARGET TISSUES.

-:- SUBCELLULAR LOCATION: Nuclear.

-:- DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN, A DNA-BINDING DOMAIN ADMAIN A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     327 HSSLSHLAVSNSTPPPATSPVSIKVKAEPQSPPRDLSPAVISRIAMVPRAGGGSSSSTSS 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      235 SPGSQ------NGRASNLRVVIPPTIAPIPPNMSAPDDVGYADQRQSQ 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              122 DILSLIGTALPPPAPPGAGGLIVYLAGGQGQVVGGNVAGSLIASGPVVLMAASFANAVYD 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            277 ISLNIPVVTLQTPIP----ALTSYSFGAQ-----DFSSSGVMNSADIMSLNIWHQGLVP 326
                                                                                                                                                                                                                                                                                                                                                                                       184 IDSGGMSLIIYPSGSMLEMSNGYPHSHSPLVGSPSPGP-----SPGI--AHHLSIKQQ 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                     72 SDISEAVSTYATRRGCGVCIISGTGAVTNVTIRQP-----AAPAGGGVITLHGRF 121
                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                            16 TPTGGATSSATASGS----SSGRRPRGRPAGSKNKPKPPTIITRDSPNVLRSHVLEVTSG 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              J. MOI. EVOL. 47:334-342(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Choong C.S., Kemppainen J.A., Wilson E.M.; "Evolution of the primate androgen receptor: a structural basis for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eulemur fulvus collaris (Collared brown lemur).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Strepsirhini; Lemuridae; Eulemur.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             182 RLPIE----EEETPPPRTTGV-----QQQQPEASQSSEVT------GSGAQACES
                          S -> R (IN REF. 2).
PAVISRIAMVPRAG -> ASGHQQNSNGSTGS (IN
                                                                                                                                                                                                                                                                     75;
                                                                                                                                                                                                          DB 1; Length 515;
                                                                                                                                                                                                                                                                        31; Mismatches 114; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         222 NLQGGNGGGG-VAFYNLGMNMNNFQFSGGDIYGMSGGSGGGGGGAT 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    387 NASGGAGGGAVSAANVITHLNNVSVLAG---GPSGQGGGGGGGGG 429
                                                                                                              832C1FB4A831F28E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Androgen receptor (Dihydrotestosterone receptor).
                                                                                                                                                                                                                                           0.43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 884 AA.
                                                                                                                                                                                                       8.9%; Score 123.5; ilarity 23.1%; Pred. No. 0.4 Conservative 31; Mismatches
POLY-GLN.
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InterPro; IPR000536; Hormone_rec_lig.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=98404153; PubMed=9732460;
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                                                                                                                     54289 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; U94178; AAC73049.1; -.
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495
338
377
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                                                                                                                        515 AA;
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                                                                                                                                                                                                                                                 Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=47178;
484
338
364
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ANDR_EULFC
                                                                                                                                                                                                                                                                                  99
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                                                                                                                        SEQUENCE
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                                CONFLICT
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   DOMAIN
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DNA_BIND
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                                                                                                                                                                                                                                                                                          12;
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                                                                                                                                                                                                                                                                                                                           170 MQLLQQQQQEAVSE------GSSSGRAREAAGAPTSSKDSYLGGTSTISDSA 215
                                                                                                                                                                                                                                                                                                                                                                                       117 LHGRFDILSLTGTALPPPAPPGAGGLTVYLAGGQGQVVGGNVAG------SLIAS 165
                                                                                                                                                                                                                                                                                                                                                                                                           275 ----DDSADKGTEEPAEYTPFKGSYTQGLEGESLGCSGSSEAGSSGTLELPSTLSLYKS 329
                                                                                                                                                                                                                                                                                                                                                                                                                                GPVVLMAASFANAVYDRLPIEEEETPPPRT----TGVQQQQPEASQSSEVTGSGAQACE 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       221 SNLQGGNGGGGV------AFYNLGMNMNNFQFSGGDIYGMSGGSGG--GGGA 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63; Gaps
                                                                                                                                                                                                                                                                                                                                                                    216 KELCKAVSVSMGLGVETLEHLSPGEQLRGDCMYAPLLGGPPAVRPTPCAPLAECKGSLL- 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                   330 G-ALEEAASYOSRDYYNFPLALAGPPPPPLPPHPHARIKLENP-LDYGSSWAAAAQCRF 387
                                                                                                                                                                                                                                                                                                       1 MELNRSEADEAKAETTPTGGATSSATASGSSSG--RRPRGRPAGSKNKPKPPTIITRDSP 58
                                              SMART; SM00430; HOLI; 1.

SMART; SM00399; ZnF_C4; 1.

PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.

Receptor; Transcription regulation; DNA-binding; Nuclear protein; Zinc-finger; Steroid-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                     DB 1; Length 884;
                                                                                                                                                                                                                                                                                         Indels
                                                                                                     MODULATING (BY SIMILARITY).
                                                                                                                                                                                                                                    18F570E352F4D2BD CRC64;
                                                                                                                NUCLEAR RECEPTOR-TYPE
                                                                                                                                                                                                                                                                 / Match 8.9%; Score 123.5; DB 1; Local Similarity 25.1%; Pred. No. 0.74; les 76; Conservative 28; Mismatches 136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Androgen receptor (Dihydrotestosterone receptor). AR OR NR3C4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
                                                                                                                                           LIGAND-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       895 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Choong C.S., Kemppainen J.A., Wilson E.M.;
                                                                                                                                                                                  POLY-GLN.
POLY-PRO.
POLY-ALA.
                                                                                                                                                                          POLY-ALA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
       Pfam: PF02166; Androgen_recep; 1. Pfam: PF00104; hormone_rec; 1. Pfam: PF00105; zf-C4; 1. PRINTS; PR00047; STROIDFINGER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-98404153; PubMed-9732460;
                                                                                                                                                                                                                                      .
MW
IPR001628; zf-C4.
                                                                                                                                                                                                                                      95610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cercopithecinae; Macaca
                                                                                                                                                                                                                                   884 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9541;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               266 TRP 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   442 VTP 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ANDR_MACFA
097952;
                                                                                                            DNA_BIND
ZN_FING
ZN_FING
                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                   SEQUENCE
                                                                                                   DOMAIN
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                          disease.";
J. Mol. Evol. 47:334-342(1998).
-!- FUNCTION: THE STEEDID HORMONES AND THEIR RECEPTORS ARE INVOLVED IN THE REGULATION OF BUKARYOTIC GENE EXPRESSION AND AFFECT CELLULAR PROLIFERATION AND DIFFERENTIATION IN TARGET TISSUES.
                                                                                                                                                                                        SUBCELLULAR LOCATION: Nuclear.
DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN,
A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.
SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
NR3 SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       59 NVLRSHV-LEVTSGSDISEAVSTYATRG-CGVCIISGTGAVTNVTIRQPAAPAGGGVIT 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       220 KELCKAVSVSMGLGVEALEHLSPGEQLRGDCMYAPVLGVPPAVRPTPCAPLAECKGSLL- 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   117 LHGRFDILSLTGTALPPPAPPGAGGLTVYLAGGQGQVVGGNVAGSLIASGPVVL---- 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           174 MOLLQQQQQEAVSE-----GSSSGRAREASGAPTSSKDNYLGGTSTISDSA 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----MAASFANAVYDRLPIEEEETPPPRT----TGVQQQQPEASQSSEVTGSGAQA 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             65; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               331 YKSGALDEAAAYOSRDYYNFPLALAGPPPPPPPPPPHPHARIKLENP-LDYGSAWAAAAQC 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MELNRSEADEAKAETTPTGGATSSATASGSSSG--RRPRGRPAGSKNKPKPPTIITRDSP 58
"Evolution of the primate androgen receptor: a structural basis for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              219 CESNLQGGNGGGGV-----AFYNLGMNMNNFQFSGGDIYGMSGGSGGGGG 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              390 RYGDLASLHGAGAAGPGSGSPSAAASSSWHTL----FTAEEGQLYGPCGGGGGGGG 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam: PF00104; horiogen_rec; 1.
Pfam: PF00105; zf-C4; 1.
PRINTS; PR00047; STROIDFINGER.
SMART; SM0039; LAF_C4; 1.
PROSITE; PS00031; NUCLEAR_ECEPTOR; 1.
PROSITE; NANOSSPECEPTOR; 1.
Receptor; Transcription regulation; DNA-binding; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8.8%; Score 122.5; DB 1; Length 895;
23.4%; Pred. No. 0.86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MODULATING (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A3EB17916F43A097 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUCLEAR RECEPTOR-TYPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23.4%; Pred. No. .....
tive 35; Mismatches 129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LIGAND-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POLY-GLN.
POLY-GLN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Haber; kudalos; luuc.
Interpro: IPR001103; Androgen_recep.
Interpro: IPR001636; Hormone_rec_lig.
Interpro: IPR001628; zf-c4.
Pfam; PF02166; Androgen_recep; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POLY-GLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POLY-PRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POLY-ALA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POLY - GLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96494 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; U94179; AAC73050.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
nes 70; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               895 AA;
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16-OCT-2001 (Rel. 40, Last annotation update)
MHC class II regulatory factor RFX1 (RFX) (Enhancer factor C) (EF-C).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR003150; RFX_DNA_binding.
Pfam; PF02257; RFX_DNA_binding; 1.
DNA-binding; Transcription regulation; Activator; Nuclear protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDILINE-94040774; PubMed-8224874; Safrany G., Perry R.P.; Safrany G., Perry R.P.; "Transcription factor ferth helps control the promoter of the mouse ribosomal protein-encoding gene rpL30 by binding to its alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Reith W., Sanohez-Herrero C., Kobr M., Silacci P., Berte C., Barras E., Mach B.; Constant C., Kobr M., Sanohez-Herrero C., Kobr M., Sanohez-Herrero C., Kobr M., Sanohez-Herrero C., Kobr M., Sanohez-Herrero C., Mach B.; 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      iDENTITY BETWEEN REX1 AND EF-C.
MEDLINE-94019311; PubMed-8413236;
Siegrist C.A., Durand B., Emery P., David E., Hearing P., Mach B.,
                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "RFX1 is identical to enhancer factor C and functions as a transactivator of the hepatitis B virus enhancer."; Mol. Cell. Biol. 13:6375-6384(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EXPERIMENTALLY DEDUCED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION: Nuclear. SIMILARITY: BELONGS TO THE RFX FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBUNIT: BINDS DNA AS AN HOMODIMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GLY-RICH
                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. MEDLINE-91071581; Pubmed-2253877;
                                                                                                                                                01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; X58964; CAA41730.1; -. EMBL; A20498; CAA01506.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BINDING TO RPL30 PROMOTER.
                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gene 132:279-283(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRANSFAC; T00909; -. TRANSFAC; T01673; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR; A35913; A35913.
                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MIM; 600006; -
                                                                          RFX1_HUMAN
P22670;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA_BIND
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                          RFX1_HUMAN
RESULT
                                                                                                                      FIRE PRESENTANT FOR PRESENTANT FRANCE FOR SECOND FOR FRANCE FRANC
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J. Mol. Evol. 47:334-342(1998).

--- FUNCTION: THE STEROID HORMONES AND THEIR RECEPTORS ARE INVOLVED IN THE REGULATION OF EUKARYOTIC GENE EXPRESSION AND AFFECT CELLULAR PROLIFERATION AND DIFFERENTIATION IN TARGET TISSUES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -i- SUBCELLULAR LOCATION: Nuclear.
-i- DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN,
A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.
-i- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
                                                                                                                                                                                                                                                                                                                                        284 QVPVPHVYSSQVQYVEGGDASYTASAIRSSTYSYPETPLYTQTASTSYYEAAGTATQVST 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          192 PPRITGVQQ--QQPEASQSSEVTGS----GAQACESNLQGGNGGGGVAFYNLGMNMNFQ 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                104 TVSEGAMRASETVSEASPGSTASQTGVPTOVVQQVQGTQQRLLVQTSVQAKPGHVSPLQL 163
                                                                                                                                                                                                                                                                                                                    224 PTGTVPQQLQVHGVQQSVPVTQERSVVQATPQAPKPGPVQPLTVQGLQPVHVAQEVQQLQ 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   145 ------YLAGGQGQVVGGNVAGSLIASGPVVLMAASFANAVYDRLPIEEETP 191
                                                                                         8.8%; Score 124; ......
20.5%; Pred. No. 1;
vative 34; Mismatches 124; Indels 144; Gaps
                                                                                                                                                                                                     44 PIAAATPQPQYVTELQSPQPQAQPPGGQKQYVTELPAVPAPSQPTGAPTPSPAPQQYIVV 103
                                                                                                                                                                  17 PIGGAISSAIASGSSSGRRPRGRPAGSKNK------PKPPTIIIRDSPNVLRSHVL 66
                                                                                                                                                                                                                                             ----- AV 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
Choong C.S., Kemppainen J.A., Wilson E.M.;
"Evolution of the primate androgen receptor: a structural basis for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
                   NECESSARY FOR DIMERIZATION. 556151F88C6AC9A2 CRC64;
                                                                                                                                                                                                                                               67 EVTSGS-DISEAVS----TYATRRGCGVCI---ISGTG-----
                                                                                                                                                                                                                                                                                                                                                                                               ----ALPPPAPPG-AGGLTV--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Androgen receptor (Dihydrotestosterone receptor).
AR OR NR3C4.
ASP/GLU-RICH (ACIDIC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Papio hamadryas (Hamadryas baboon)
                                           104728 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               392 -GGGGGGGGGSGSTGGGGSGA 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           246 FSGGDIYGMSGGSGGGGGA 265
                                                                                                                                      78; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cercopithecinae; Papio.
     920
744
979 AA;
                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NR3 SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9557;
                                                                                                                                                                                                                                                                                                                                                                                                     126 LTGT-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ANDR_PAPHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    disease.";
                           DOMAIN
SEQUENCE
           DOMAIN
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                                                                                                                                          Matches
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entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                        11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              279 -----DDSAGKSTEDTAEYSPFKGG---YTKGLEGESLGCSGSAAAGSSGTLELPSTLSL 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                         220 KELCKAVSVSMGLGVEALEHLSPGEQLRGDCMYAPVLGVPPAVRPTPCAPLAECKGSLL- 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 117 LHGRFDILSLTGTALPPPAPPGAGGLTVYLAGGQGQVVGGNVAGSLIASGPVVL----- 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----MAASFANAVYDRLPIEEEETPPPRT----TGVQQQQPEASQSSEVTGSGAQA 218
                                                                                                                                                                                                                                                                                                                                                                                                               174 MQLLQQQQQEAVSE-----GSSSGRAREASGAPISSKDNYLGGISIISDSA 219
                                                                                                                                                                                                                                                                                                                                                                                                                                      59 NVLRSHV-LEVTSGSDISEAVSTYATRRG-CGVCIISGTGAVTNVTIRQPAAPAGGGVIT 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 331 YKSGALDEAAAYOSRDYYNFPLALAGPPPPPPPPPHPHARIKLENP-LDYGSAWAAAAQC 389
                                                                                                                                                                                                                                                                                                                                                                        65; Gaps
                                                                                                                                                                                                                                                                                                                                                                                         1 MELNRSEADEAKAETTPTGGATSSATASGSSSG--RRPRGRPAGSKNKPKPPTIITRDSP 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      219 CESNLQGGNGGGGV------AFYNLGMNMNNFQFSGGDIYGMSGGSGGGGG 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           390 RYGELASLHGAGAAGPGSGSPSAAASSSWHTL----FTAEEGQLYGPCGGGGGGGG 442
                                                                                                        Pfam; PF00105; Zf-C4; I.
PRINTS; PR00047; STROIDFINGER.
SMART; SM00399; ZnF_C4; 1.
PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
Receptor; Transcription regulation; DNA-binding; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pan troglodytes (Chimpanzee).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
                                                                                                                                                                                                                                                                                                                                                Length 895;
                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                       MODULATING (BY SIMILARITY). NUCLEAR RECEPTOR-TYPE.
                                                                                                                                                                                                                                                                                                               9020C0DC67F11E5D CRC64;
                                                                                                                                                                                                                                                                                                                                               8.7%; Score 121.5; DB 1;
23.4%; Pred. No. 0.99;
Live 34; Mismatches 130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Androgen receptor (Dihydrotestosterone receptor).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                  LIGAND-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE-98404153; PubMed-9732460;
Choong C.S., Kemppainen J.A., Wilson E.M.;
                                                                                                                                                                                                            C4 -TYPE.
C4 -TYPE.
                                                                                                                                                                                                                                                                   POLY-GLN.
POLY-PRO.
                                                                                                                                                                                                                                             POLY-GLN
                                                                                                                                                                                                                                                                                          POLY-ALA
                                                                                                                                                                                                                                                                                                      POLY-GLY
                                                   InterPro; IPR001103; Androgen_recep.
InterPro; IPR000536; Hormone_rec_lig.
InterPro; IPR001628; zf-C4.
                                                                                    Pfam; PF02166; Androgen_recep; 1. Pfam; PF00104; hormone_rec; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ANDR_PANTR STANDARD; 1097775;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequ
30-MAY-2000 (Rel. 39, Last anno
                                                                                                                                                                                                                                                                                                                 MW;
                                                                                                                                                                             inc-finger; Steroid-binding.
                              EMBL; U94176; AAC73047.1; -. HSSP; P06536; 1GDC.
                                                                                                                                                                                                                                                                                                                 96478
                                                                                                                                                                                                                                                                                                                                                                     70; Conservative
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595
895
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895 AA;
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Best Local Similarity
Matches 70; Conser
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBCELLULAR LOCATION: Nuclear.

DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN, A DNA BINDING DOMAIN A C-TERMINAL STEROID-BINDING DOMAIN.

SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   59 NVLRSHV-LEVTSGSDISEAVSTYATRRG-CGVCIISGTGAVTNVTIRQPAAPAGGGVIT 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      234 KELCKAVSVSMGLGVEALEHLSPGEQLRGDCMYAPLLGVPPAVRPTPCAPLAECKGSLL- 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       117 LHGRFDILSLTGTALPPPAPPGAGGLTVYLAGGOGQVVGGNVAGSLIASGPVVL---- 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    293 ----DDSAGKSTEDTAEYSPFKGG---YTKGLEGESLGCSGSAAAGSSGTLELPSTLSL 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       171 -----MAASFANAVYDRLPIEEEETPPPRT-----TGVQQQQPEASQSSEVTGSGAQA 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         345 YKSGALDEAAAYQSRDYYNFPLALAGPPPPPPPPPPHPHRIKLENP-LDYGSAWAAAAQC 403
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"Evolution of the primate androgen receptor: a structural basis for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF02166; Androgen_recep; 1.
Pfam; PF00104; hormone_rec; 1.
Pfam; PF00105; 2F-C4; 1.
PRINTS; PR00047; STROIDFINGER.
SWART; SW00399; ZnF_C4; 1.
PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
Zinc-finger; Steroid-binding.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MODULATING (BY SIMILARITY)
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POLY-ALA.
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INTERPRO; IPRO01103; Androgen_recep.
InterPro; IPR001638; HORmone_rec_lig.
InterPro; IPR001628; zf-C4.
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MEDLINE-88240407; PubMed=3377788;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chang C., Kokontis J., Liao S.; "Structural analysis of complementary DNA and amino acid sequences of
                                                                                                                                                                                                                                                             SEQUENCE FROM N.A., AND VARIANT CAIS MET-866.

Lubahn D.B., Brown T.R., Simental J.A., Higgs H.N., Migeon C.J.,
Wilson E.M., French F.S.

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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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AR OR NR3C4 OR DHTR.
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                        919 AA.
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                        PRT;
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MEDLINE=89098909; PubMed=2911578;
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                                                                                                                                                                                 MEDLINE=89112208; PubMed=3216866;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=89017168; PubMed=3174628;
                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=90258935; PubMed=2342476;
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                                               01-MAR-1989 (Rel. 10, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Science 240:324-326(1988).
                        STANDARD;
                                                                                                           Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                       ANDR_HUMAN
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                                     P10275
             ANDR_HUMAN
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REVIEW ON VARIANTS.
MEDLINE-95352489; PubMed-7626493;
Brinkmann A.O., Jenster G., Ris-Stalpers C., van der Korput J.A.G.M.,
Trapman J., Klaassen P., Kuiper G.G.J.M., van der Korput J.A.G.M., Faber P.W., van Rooij H.C.J., Geurts van Kessel A., Voorhorst M.M., Mulder E., Brinkmann A.O.;
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MEDLINE=97250535; PubMed=9096391;
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"Trinucleotide repeat polymorphism in the androgen receptor gene
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Brown T.R., Scherer P.A., Chang Y.-T., Migeon C.J., Ghirri P.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-93092459; PubMed-1458719;
Pinsky L., Trifiro M.A., Kaufman M., Beitel L.K., Mhatre A.,
Kazemi-Esfarjani P., Sabbaghian N., Lumbroso R., Alvarado C.,
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Sultan C., Lumbroso S., Poujol N., Belon C., Boudon C.,
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Eur. J. Pediatr. 152 Suppl. 2:862-869(1993).
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response to anti-androgens.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          235 KELCKAVSVSMGLGVEALEHLSPGEQLRGDCMYAPLLGVPPAVRPTPCAPLACKGSLL- 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Androgen resistance associated with a mutation of the androgen receptor at amino acid 772 (Arg.->Cys) results from a combination of decreased messenger ribonucieic acid levels and impairment of receptor function.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59 NVLRSHV-LEVTSGSDISEAVSTYATRRG-CGVCIISGTGAVTNVTIRQPAAPAGGGVIT 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MELNRSEADEAKAETTPTGGATSSATASGSSSG--RRPRGRPAGSKNKPKPPTIITRDSP 58
                                                                                                                                                                                                                                                                                                                                                                                                                                          Corfen J.L.;
Functional characterization of naturally occurring mutant androgen
receptors from subjects with complete androgen insensitivity.";
Mol. Endocrinol. 4:1759-1772(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A mutation in the DNA-binding domain of the androgen receptor gene causes complete testicular feminization in a patient with receptor-positive androgen resistance.";
                                                                    REVIEW ON VARIANTS.
MEDLINE-97169385; PubMed-9016528;
Gottlieb B., Trifiro M.A., Lumbroso R., Vasiliou D.M., Pinsky L.;
The androgen receptor gene mutations database.";
Nucleic Acids Res. 25:158-162(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                    Brown T.R., Lubahn D.B., Wilson E.M., French F.S., Migeon C.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-91310758; PubMed-1856263;
Marcelli M., Tilley W.D., Zoppi S., Griffin J.E., Wilson J.D.,
McPhaul M.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Marcell1 M., Zoppi S., Grino P.B., Griffin J.E., Wilson J.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8.5%; Score 118.5; DB 1; Length 919; 23.1%; Pred. No. 1.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   36; Mismatches 129;
Bruggenwirth H.T., Boehmer A.L.M., Trapman J.;
"Androgen receptor mutations.";
J. Steroid Blochem. Mol. Biol. 53:443-448(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     receptor function.";
J. Clin. Endocrinol. Metab. 73:318-325(1991).
                                                                                                                                                                                                                                                                                                                                                                                 VARIANTS CAIS CYS-774; GLN-831 AND MET-866.
MEDLINE-91186983; PubMed-2082179;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-91154385; PubMed-1999491;
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Matches 69; Conserv
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"BETA3, a novel helix-loop-helix protein, can act as a negative
"ETA3, a novel helix-loop-helix protein, can act as a negative
"Caulator of BETA2 and MyoD-responsive genes.";
"Locall Biol. 16:626-633(1996).
"Cell Biol. 16:626-633(1996).
"Cell Biol. 18:020-BETA2 BA31 BIOLING OF TOTS AS A STRONG REPRESSOR OF
"RERADIA NOND-RESPONSIVE GENES, PROBABLE BY HETERODIMERIZATION
"MITH CLASS A BASIC HELIX-LOOP-HELIX PACTORS. DESPITE THE PRESENCE
"COF AN INTACT BASIC DOMAIN, DOES NOT BIND TO DNA.
"SUBUNITH HETERODIMER MITH OTHER BILL PROTEINS, LIKE TOTS (E47).
"CI- SUBUNITH HETERODIMER MITH OTHER PROTEINS, LIKE TOTS (E47).
"CI- SUBCELLULAR LOCATION: NUCLEAR (POCHALLA).
"CI- SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY OF
"TRANSCRIPTION FACTORS." ATONAL" SUBERMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         between the Swiss Institute of Bloinformatics and the EMBL outstation. The European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                        346 YKSGALDEAAAYQSRDYYNFPLALAGPPPPPPPPPPPHPHARIKLENP-LDYGSAWAAAAAQC 404
------MAASFANAVYDRLPIEEEETPPPRT-----TGVQQQQPEASQSSEVTGSGAQA 218
                                                                         219 CESNLQGGNGGGGV-----AFYNLGMNMNNFQFSGGDIYGMSGGSGGGGG 264
                                                                                                     405 RYGDLASLHGAGAAGPGSGSPSAAASSSWHTL-----FTAEEGQLYGPCGGGGGGG 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           65; Indels 142; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Peyton M., Stellrecht C.M.M., Naya F.J., Huang H.-P., Samora P.J.,
                                                                                                                                                                                                                                                                                                                       Mesocricetus auratus (Golden hamster).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ch 8.4%; Score 117; DB 1; Length 367; 1 Similarity 23.3%; Pred. No. 0.77; 68; Conservative 17; Mismatches 65; Indels 1.
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InterPro; IPR001092; HLH_dim.
Pfam; PF00010; HLH; 1.
PROSITE; PS00038; HELIX_LOOP_HELIX; 1.
Nuclear protein; Transcription regulation; Repressor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6CAB9AFF96E85F77 CRC64;
                                                                                                                                                                                                                                           30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                             367 AA.
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POLY-GLY.
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                                                                                                                                                                                                           PRT;
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                                                                                                                                                                                                             STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID-10036;
                                                                                                                                                                                                                                                                                                      BETA3 protein.
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                                                                                                                                                                                                         BET3_MESAU
009029;
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SINGLELANDOUS: THE SEGMENT H5 IS THOUGHT TO LINE THE CHANNEL PORE.

SINILARITY: TO THE MEMBERS OF THE POTASSIUM CHANNEL PROTEINS
OF THE SH SUPERFAMILY.

SIMILARITY: CONTAINS I CYCLIC NUCLEOTIDE-BINDING DOMAIN.

SIMILARITY: CONTAINS I PAS (PER-ARNT-SIM) DIMERIZATION DOMAIN.

SIMILARITY: CONTAINS I PAS-ASSOCIATED C-TERMINAL (PAC) DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pteryyota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBGNIT: DIMER (POTENTIAL).
SUBCELLUIAL LOCATION: Integral membrane protein.
MISCELLANGOUS: THE SEGMENT S4 IS PROBABLY THE VOITAGE-SENSOR AND
IS CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
                                                                                                                                                                                                                                                                                                                                     128 CLKYGESAGRGSVAESSGGEQSPDDDSDGRCELVLRAGGADPRASPGA--GGGGTKVVEG 185
                                                         SGSDISEAVSTYATRRGCGVCIISGTGAVTNVTIRQPAAPAGGGVITLHGRFDILSLTGT 129
                                                                                                                                                                 130 ALPPPAPPGAGGLTVYLAGGQGQVVGGNVAGSLIASGPVVLMAASFANAVYDRLP---- 184
                                                                                                                                                                                                         Science 252:1560-1562(1991).
-!- FUNCTION: PROTEIN EAG IS MOST PROBABLY A STRUCTURAL COMPONENT OF
THE POTASSIUM CHANNEL AND MEDIATES THE POTASSIUM PERMEABILITY OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

BEDLINE-S1262655; bubmed-1840699; marker J., Drysdale R., Ganetzky B.; marker J., Drysdale R., Ganetzky B.; "A distinct potassium channel polypeptide encoded by the Drosophila
                                                                                                                                                                                                                                                                              ----IEE----EETPPPRTTG-----VQQQQPEASQSSEVTGSGAQACE-
                                                                                                                                                                                                                                                                                                                                                                                            221 ---SNLQGGNG---GGGVAFYNLGMNMNNFQFSGGDIYGMSGGSGGGGGGAT 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                186 CSNAHLHGGAGLPPGGSTG-----SGG-----GGSGGGGGGGS 218
                                                                                                                ----FEPADPEGAGLL----
     34 EAAFRSTPPGMDLSLAPP-----PRERPASSSSP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
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InterPro: IPR000635; Cation_chan_non_lig.
InterPro: IPR001620; Channel_pore_K.
InterPro: IPR0001610; PAC.
InterPro: IPR000700; PAS-assoc_C.
InterPro: IPR000014; PAS-
InterPro: IPR000014; CNMP_binding.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequ
16-OCT-2001 (Rel. 40, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Potassium channel protein eag.
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973 -SAVTSPVDTVITISSPGA---SGSGSGTGAGAGSAVAGAGGAGLLDPGATVVSSAGGNG 1028
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          177 NAVYDRLPIEEEETPPPRTTGVQQQQPEASQSSEVTGSGAQACESNLQGGNGGGGVAFYN 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     71 GSDISEAVSTYATRRGCGVCIISGTGAVTNVTIRQPAAPAGGGVITLHGRFDILSLTGTA 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  932 GASSGGNAPDNSSGQTTPGDEICAGCGAGGGGTPTTQAPPT--------972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20 GATSSATASGSSSGRRPRGRP-----AGSKNKPKPPTIITRDSPNVLRSHVLEVTS 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Araki E., Haag B.L. III, Kahn C.R.; "Cloning of the mouse insulin receptor substrate-1 (IRS-1) gene and complete sequence of mouse IRS-1."; Biochim. Biophys. Acta 1221:353-356(1994).
                                                                                                                                                 lonic channel; Transmembrane; Ion transport; Voltage-gated channel;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
Ww. 344C80DC06E4340E CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8.4%; Score 117; DB 1; Length 1174; 11.6%; Pred. No. 2.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94; Indels
                                                                                                                                                                                   SEGMENT S1 (POTENTIAL).
SEGMENT S2 (POTENTIAL).
SEGMENT S3 (POTENTIAL).
SEGMENT S4 (POTENTIAL).
SEGMENT S5 (POTENTIAL).
SEGMENT S5 (POTENTIAL).
SEGMENT S6 (POTENTIAL).
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01-UNN-1994 (Rel. 29, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
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+ive 23; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               237 LGMNMNNFQFSGGDIYGMSGGSGGGGGA 265
                                                                                          PROSITE; PS50042; CNMP_BINDING_3; 1. PROSITE; PS50112; PAS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE=94220494; Pubmed=8167159;
                                                                                                                                                                                                                                                                                                                                                                    CNMP
                                                                                                                                                                                                                                                                                                                                                                                                                                             126236 MW;
                                                                                                                                                                         Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Insulin receptor substrate-1.
IRS1 OR IRS-1.
Pfam; PF00520; ion_trans; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                   PROSITE; PS50113; PAC; 1
                                  SMART; SM00086; PAC; 1.
SMART; SM00091; PAS; 1.
SMART; SM00100; CNMP; 1.
                                                                                                                                                                                                                                 335
369
369
467
493
165
688
688
412
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                                                                                                                                                                                                                                                                                                                                                                                                                           424 47
1174 AA;
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                                                                                                                                                                                                                               314
343
372
442
471
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1113
571
262
412
                                                                                                                                                                           Glycoprotein;
TRANSMEM 22
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P35569;
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CARBOHYD
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Best Local 3
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16;
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                                                                                                                                                                                                                                        785 RLSSSSGRLRYTATAEDSSSSTSSDSLGGGYCGARPESSLTHP-------HHH 830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             65 VLEVTSGSDISEAVSTYA-----TRRGCGVCIISGTGAVTNVTIRQ-------PAAP 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels 131; Gaps
                                                       RSEADEAKAETTPTGGATSSATASGSSSGRRPRGRPAGSKNKPKPPTIITRDSPNVLRSH
          Keller S.R., Aebersold R., Garner C.W., Lienhard G.E.; "The insulin-elicited 160 kDa phosphotyrosine protein in mouse adipocytes is an insulin receptor substrate 1: identification by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1233;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             H -> R (IN REF. 2).
W; COE9B2D890DADD87 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (BY SIMILARITY).
PHOSPHORYLATION (BY INSR)
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PHOSPHORYLATION (BY INSR)
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PHOSPHORYLATION (BY INSR)
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PHOSPHORYLATION (BY INSR)
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PHOSPHORYLATION (BY INSR)
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PHOSPHORYLATION (BY INSR)
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MISSING (IN REF. 2).
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8.4%; Score 116.5; DB 1;
Best Local Similarity 22.8%; Pred. No. 2.8;
Matches 84; Conservative 29; Mismatches 125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (BY SIMILARITY
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InterPro; IPR002404; Insulin_Recep_S-l.
InterPro; IPR001849; PH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          POLY-GLN.
POLY-GLY.
POLY-PRO.
MEDLINE-93192326; PubMed-8448209;
                                                                                                                                                                                                                                                                                                                                  Pfam: PF02174; IRS; 1.
Pfam: PF00169; PH; 1.
PRINTS; PR00628; INSULINESI.
SMART; SM00310; PH; 1.
PR0STIE; PS50003; PH_DOMAIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1038 1039 MIS;
1182 1182 H -:
1233 AA; 130723 MW;
                                                                                                                                                                                                                                                  EMBL; L24563; AAA39335.1; -. EMBL; X69722; CAA49378.1; -. PIR; S43514; S43514.
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                                                                                                                                                                                        1004 VSYADM---RTGIAAEKASLPRPTGAAPPPSSTASSSASVTPQGATAEQATHSSLLGGPQ 1060
                                                                                                                                                                                                                                                      1061 GPGGMSAFTRVNLSPNHNQSAKVIRADTQGCRRRHSSETFSAPTRAGNTVPFGAGAAVGG 1120
                                                                                                                946 ATWQESGGVELGRIGPAPPGSATVCRPTRSVPNSRGDYMTWQIGCPRQSYVDTSPVA--P 1003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      228 GGGGV-AFYNLGMNMNNFQ------GG 257
831 VLQPHLPRKVDTAAQTNSRLARPTRLSLG-----DPKASTLPRVREQQQQQQSSLHPPEP 885
                               110 AGGGVIT-------LHGRFDILSLTGTALPP--------------------------133
                                                                                            173 ASFANAVYDRLPIEEEETPPPRTTG-VQQQQPEASQSSEVTGSGA---QACESNLQGG-N 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDINE-91117256; PubMed-1703632; MEDINE-91117256; PubMed-1703632; Voelker R.A., Gibson W., Graves J.P., Sterling J.F., Elsenberg M.T.; "The Drosophila suppressor of sable gene encodes a polypeptide with repions similar to those of RNA-binding proteins."; MOI. Cell. Biol. 11:894-905(1991).
                                                             886 KSPGEYVNIEFGSGQPGYLAGPATSRSSPSVRCPPQLHPAPREETGSEEYMNMDLGPGRR
                                                                                                                                                                                                                                                                                                                                                                                                                                 01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                    PRT; 1322 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster (Fruit fly)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR; A39612; A39612.
FlyBase; FBgn0003575; su(s).
InterPro; IPR000571; zf-CCCH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; M57889; AAA28920.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; X59364; CAA42010.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Suppressor of sable protein.
                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                       1121 SGGGGGGGS 1129
                                                                                                                                                                                                                                                                                         SGGGGGGAT 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-OREGON-R
                                                                                                                                                                                                                                                                                                                                                                                                  SUS_DROME P22293;
                                                                                                                                                                                                                                                                                                                                                                      RESULT 14
SUS_DROME
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Search completed: July 10, 2002, 22:31:08
Job time: 585 sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 48:311-319(1987).

DOMAIN: THERR ARE 10 TANDEM COPIES OF 9 - RESIDUE REPEAT (PRECEDED BY A 6-RESIDUE REPEAT) AND 3 TANDEM COPIES OF A 16-RESIDUE REPEAT (FOLLOWED BY 3 SHORTER, INCOMPLETE COPIES).

RESIDUE REPEAT (FOLLOWED BY 3 SHORTER, INCOMPLETE COPIES).

SURFACE ANTIGEN ON THE SPORGOTTE (THE INFECTIVE STAGE OF THE MALARIA PARASITE THAT IS TRANSMITTED FROM THE MOSQUITO TO THE
                                                                                                                                                                                                                                                                                                     1036 PTKGASTANTTAPNASG------GSK-------QISEIRSLLQVSN 1068
                                                                                                                                                                                                                                                                                                                                                                                         1069 WYNNLGTNNKIMVNQQLALVFTELKKFHQLPNDAPKIFDVSFIVNNTTLQQIFAKL---- 1124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1125 -----FIFVDDNGEVVQIPEEPNGNGAALGGGGDSGGGGGGGG-----GGVVLPNLS 1173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1174 OPPPNLSOM----LRLPPPNIRMLRMSGMMMOMGNVGPPFNOPPRGGLMGMPPNGNGLN 1229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1230 QGVGNLGGLGQLGINQGGGPVPNGNPFNPFGGNNGGGAGVMNNMNSMGNMGMGFNNFNNN 1289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       175 FANAVYDRLPIEEEETPPP----RTTGVQQQQ----PEASQ-----SSEVTGSGAQ 217
                                                                                                                                                                                                                                                                                                                                                 77 AVSTYATRRGCGV------CIISGTGAVTNVIIRQPAAPAGGGV 114
                                                                                                                                                                                                                                                                                                                                                                                                                                  115 ITLHGRFDILSLTGTALPPPAPPGAGGLTVYLAGGQGQVVGGNVAGSLIASGPVVLMAAS 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---GGNGGGGV-----AFYNLGMNMNNFQFS 247
                                                                                                                                                                                                                                                            17 PTGGATSSATASGSSSGRRPRGRPAGSKNKPKPPTIITRDSPNVLRSHVLEVTSGSDISE 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- MISCELLANEOUS: THE C-TERMINAL REGION IS PROBABLY USED FOR ANCHORING THE PROTEIN TO THE CELL MEMBRANE. THE REPEAT SEQUENCES WOULD BE THE SURFACE ANTIGEN OF THE ORGANISM.
-!- SIMILARITY: CONTAINS 1 TSP TYPE-1 DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "The circumsporozoite gene of the Plasmodium cynomolgi complex.";
                                                                                                                                                                        8.3%; Score 116; DB 1; Length 1322;
22.1%; Pred. No. 3.2;
tive 26; Mismatches 108; Indels 116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Circumsporozòite protein precursor (CS).
Plasmodium cynomolgi (strain Berok).
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                        HIGHLY CHARGED DOMAIN.
GLN-RICH (OPA-REPEAT).
RNA-BINDING (BY SIMILARITY).
MW; D5F534EB5702EA08 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Galinski M.R., Arnot D.E., Cochrane A.H., Barnwell J.W.,
Nussenzweig R.S., Enea V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Rel. 06, Created)
(Rel. 06, Last sequence update)
(Rel. 40, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-87102878; PubMed-3802196;
                                                        446 474 GLN
1087 1162 RNA
1322 AA; 143555 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               248 GG-DIYGMSGGSGGGGGATR 267
                  RNA-binding; Nuclear protein. DOMAIN 138 327
Pfam; PF00642; zf-CCCH; 2
                                                                                                                                                                                                                   71; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
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                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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P08672;
                                                                                                        SEQUENCE
                                                                                                                                                                          Query Match
                                                             DOMAIN
DOMAIN
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CSP_PLACE
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                                                                                                                                                                                                                                                                                                                                                                                                             66 LEVTSGSDISEAVSTYATRRGCGV-CIISGTGAVTNVTIRQPAAPAGGGVITLHGRFDIL 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   125 SLTGTALPPPAPPGAGGLTVYLAGGQGQVVGGNVAGSLIASGPVVLMAASFANAVYDRLP 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7 EADEAKAETIPTG-GATSSATASGSSSGRRPRGRPAGSKNKPKPPTIITRDSPNVLRSHV 65
                                                                                                                                                                                                                                                                                                                                                                                                                                       ------AAPAGDGAPAAPAGDGA-----PAAPAGDGA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           185 IEEEETPPPRITGVQQQQPEA--SQSSEVTGSGAQACESNLQGGN--GGGGVAFYNLGMN
                                                                                                                                                                                                                                                                                       8.3%; Score 115.5; DB 1; Length 378; 4.2%; Pred. No. 0.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 -----PAAPAGDGAPAGNRAGGO-PAAGGNQAGGNRAGG------
                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                               36286 MW; 779BA081C140793F CRC64;
                                                                                                                                                            CIRCUMSPOROZOITE PROTEIN.
                                                                                                                                                                          10.5 X 9 AA REPEATS.
3 X 16 AA TANDEM REPEATS.
                                                                                                                                                                                                                                                                                                                       66
                                                                                                                                                                                                                                                                                                                       9; Mismatches
send an email to license@isb-sib.ch)
                                                                                                                                              PROBABLE.
                                                                                  Pfam; PF00090; tsp_1; 1.
PRINTS; PRO1303; CRCMSPRZOITE.
SMART; SMO0209; TSP1; Repeat; Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241 MNNFQFSGDIYGMSGGSGGGGGA 265
                                         PIR; D26255; OZZQAB.
InterPro; IPR003067; Crcmsprzoite.
InterPro; IPR000884; TSP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 257 QAGAQAGGANAGNKKAGEAGGNAGA 281
                           EMBL; M15104; AAA29532.1; -.
                                                                                                                                                                                                                                                                                                      24.28;
                                                                                                                                                                                                                                                                                                                       64; Conservative
                                                                                                                                                                                      193
241
252
261
378 AA;
                                                                                                                                                                                                                                                                                                         Similarity
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SEQUENCE
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                                                                                                                                                                           DOMAIN
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Page 13

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Similarity
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                                                LRSHVLEVTSGSDISEAVSTYATRRGCGVCIISGTGAVTNVTIRQPAAPAGGGVITLHGR 120
                                                               121 FDILSLTGTALPPPAPPGAGGLTVYLAGGQGQVVGGNVAGSLIASGPVVLMAASFANAVY 180
                                                                                                              181 DRLPIEEEETPPPRTTGVQQQQPEASQSSEVTGSGAQACESNLQGGNGGGGVAFYNLGMN 240
                                                                                                                                                                 Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 MELNRSEADEAKAETTPTGGATSSATASGSSSGRRPRGRPAGSKNKPKPPTIITRDSPNV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67 EVTSGSDISEAVSTYATRRGCGVCIISGTGAVTNVTIRQPAAP-----AGGGVITLHG 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           120 RFDILSLIGTALPPPAPPGAGGLTVYLAGGQGQVVGGNVAGSLIASGPVVLMAASFANAV 179
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A Altafil H., Araujo K., Hulzar L., Rowley D., Buehler E., Dunn P.,
A Altafil H., Araujo K., Hulzar L., Rowley D., Buehler E., Dunn P.,
Gonzalez A., Krementskaia I., Kim C., Lenz C., Li J., Liu S.,
Luros S., Schwartz J., Shinn P., Toriumi M., Vysotskaia V.S.,
Malker M., Yu G., Ecker J., Theologis A., Davis R.W.;
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF194974; AAF07197.1;
R EMBL; AC007369; AA207197.1;
R EMBL; AC007369; AA207197.1;
R EMBL; SWART; SW0084; AT_hook.
Pfam: PF02178; AT_hook:
R Fam: PF02178; AT_hook:
R SWART; SW00384; AT_hook:
SEQUENCE 311 AA: 31842 MW; A80B445C9776EB7D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        50.8%; Score 706.5; DB 10; Length 311;
53.0%; Pred. No. 5e-41;
11ve 25; Mismatches 56; Indels 53; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EADEAKAETTPTGGATSSATASGSSSGRRPRGRPAGSKNKPKPPTIITRDSPNVLRSHVL 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Weigel D., Ahn J.H., Blazquez M.A., Borevitz J., Christensen S.K., Fankhuser C., Ferrandiz C., Kardailsky I., Neff M.M., Nguyen J.T., Sato S., Wang Z., Xia Y., Dixon R.A., Harrison M.J., Lamb C.J., Tancfeky M.F., Chory J., "Activation Tagging in Arabidopsis."; Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                    241 MNNFQFSGGDIYGMSGGSGGGGGGATRPAF 270
                                                                                                                                                                                                                 241 MNNFQFSGGDIXGMSGGSGGGGGATRPAF 270
                                                                                                                                                                                                                                                                                                                    01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel, 13, Last seq
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MEDLINES 9812113; PubMed-9461215;
Revan M., Bancroft I., Bent E., Love K., Goodman H., Dean C.,
Revan M., Bancroft I., Bent E., Love K., Goodman H., Dean C.,
Revan M., Bancroft I., Bent E., Love K., Goodman H., Dean C.,
Revan M., Bancroft I., Weltzenegger T., Pohl T.M., Terryn N.,
Redler E., Wambutt R., Weitzenegger T., Pohl T.M., Terryn N.,
Relen J., Villarroel R., De Clerck R., van Montagu M., Lecharny A.,
Ruborg S., Gy I., Kreig M., Lao N., Kavanagh T., Hempel S., Kotter P.,
Rantian K.D., Rieger M., Schaeffer M., Funk B., Mueller-Auer S.,
Rantian K.D., Rieger M., Schaeffer M., Funk B., Mueller-Auer S.,
Rantian K.D., Harzopoulos P., Piravandi E., Obermaler B.,
Rantibert H., Duesternfoft A., Moores T., Jones J.D.G., Eneva T.,
Rantibert H., Deusternfoft A., Moores T., Jones J.D.G., Eneva T.,
Rantibert H., Volckaert G., Mewes H.W., Klosterman S.,
Robeller C., Chalwatzis N.;
Rantidopsis challana ".,
Rathidopsis thallana";
YDRLPIEEEETP-----PPRTTGVQQQPEASQSSEVTGSGAQACESNLQGGNG 228
                                                                                                                                               239 FERLPIEEEEEEGGGGGGGGGGPPO----MOQAPSASPPSGVTGGGO-----LGGNV 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 134 PAPPGAGGLTVYLAGGQGQVVGGNVAGSLIASGPVVLMAASFANAVYDRLPIEEEETPPP 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         194 RTTGVQQQPEASQSSEVTGSGAQACESNLQGGN-----GGGGVAFYNLGMNMN-NF 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             43; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19 GGATSSATASGSSS----GRRPRGRPAGSKNKPKPPTIITRDSPNVLRSHVLEVTSGSD 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           46.4%; Score 646.5; DB 10; Length 292;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          47; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SECUENCE FROM N.A.
EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; 297344; CAB10560.1;
EMBL; AL161547; CAB78783.1;
                                                                                                                                                                                                          229 GGGVAFYNLGMNMNNFQFSGGDIYGMSGGS---GGGGGGATRPAF 270
                                                                                                                                                                                                                                                                     288 GG------YGFSGDPHLLGWGAGTPSRPPF 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical protein.
SEQUENCE 292 AA; 29724 MW; 2A948700FA543C4F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 29.7 KDA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .9e-37;
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(without alignments)
450.508 Million cell updates/sec
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                                                                                   July 10, 2002, 22:19:08; Search time 103.68 Seconds
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	O65489 arabidopsis		023620 arabidopsis	Q9c9k7 arabidopsis	Q9sr17 arabidopsis	022130 arabidopsis	Q9sz70 arabidopsis	082166 arabidopsis	049662 arabidopsis	Q91zx7 arabidopsis	Q9m2s3 arabidopsis	Q9sjg4 arabidopsis		Q9m9r4 arabidopsis		Q91vb0 arabidopsis
	QI	065489	098709	023620	09C9K7	09SR17	022130	098270	082166	049662	7x2.190	09M2S3	098364	09LTA2	09M9R4	0941Y9	Q9LVB0
	h DB	0 10	1 10	2 10	2 10	5 10	7 10	0	. r	10	10		7 10	9 10	6 10	5 10	4 10
	Lengt	27	31	29	30	3.5	3.1	3.5	200	3.5	200	3 6	25	27	20	26	404
æ	Query Match Length DB	100.0	50.8	46.4	46.4	4.5	45.2	0 77	777		41.5	, , , ,	100	35.0	30.0	29.2	20.8
	Score	1392	706.5	646.5	645.5	637.5	. 000	7.10	616	200	000	100	1 V	4000	417	407	289.5
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Q9XHY4	O9AYM0	094F52	022812	023142	OPFHMS	095433	092.RR7	049658	OGFIR	004696	049350	010750	004695	00403	7,000	049694	098273	080834	09SR16	081321	09M2D3	098302	688060	023057	O9N1PO	09GUB5	023347	053212	002KOB	C2475C
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289	283	282	274	7.0	7 7 7 7	0.407	2000	200.0	0.00	7.047	240.5	243	243	247.0	239.5	239	227	225	221	222	2115	162.5	148	146	113.5	130	100	130.3		136.5
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ALIGNMENTS

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SEQUENCE FROM N.A.
Bevan M., Hilbert H., Braun M., Holzer E., Brandt A., Duesterhoeft A.,
Hohelsel J., Jesse T., Heijnen L., Vos P., Mewes H.W., Mayer K.F.X.,
Schueller C.;
                                                    01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-DE-2010 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 26.8 KDA PROTEIN.
P23E12.50 OR AT4G35390.
Arabidopsis thaliana (Mouse-ear cress).
Arabidopsis thaliana (Mouse-ear cress).
Sexmatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 1392; DB 10; Length 270; 100.0%; Pred. No. 4.7e-88; tive 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
Hilbert H., Braun M., Holzer E., Brandt A., Duesterhoeft A.,
Hilbert H., Braun M., Mayer K.F.X.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AL022604; CAA18730.1; -.
EMBL; AL161587; CAB80256.1; -.
                                                                                                                                                                                                                                                                                                              Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
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                            PRT; 270 AA.
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Best Local Similarity 100.C
Matches 270; Conservative
                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein. SEQUENCE 270 AA; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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RY SEQUENCE FROM N.A.

RY PADLINE-21016719; PubMed-11130712;

RA THOOLOGIS A., ECKET J.R., Palm C.J., Federspiel N.A., Kaul S.,

RA THOOLOGIS A., CARCH J.R., Palm C.J., Federspiel N.A., Kaul S.,

RA White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,

RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,

RA Ching M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,

RA Dunn P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,

RA Gill J.E., Goldsmith A.D., Hass B., Hansen N.F., Hughes B., Huizar L.,

RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,

RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,

RA Miltscher J., Miranda M., Nguyen M., Nachran W.C., Osborne B.I.,

RA Miltscher J., Miranda M., Nguyen M., Rooney T., Rowley D.,

RA Sun H., Tallon L.J., Tambunga G., Tortumi M.J., Town C.D.,

RA Sun H., Tallon L.J., Tambunga G., Tortumi M.J., Town C.D.,

RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;

RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;

RA Wu D., Xu G., Fraser C.M., Venter J.C., Davis R.W.;

RA Halls.
                                                                                                                                                                                                                                            Arabidopsis thaliana (Mouse-ear cress),
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis,
 236 -----QQQQ------LGGGSNG-----GGNLFPEVAAGGGGGLPFFNLPMNMQPNV 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SSGADIVESVITYARRRGRGVSILSGNGTVANVSLROPATTAAHGANGGTGGVVALHGRF 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TSGSDISEAVSTYATRRGCGVCIISGTGAVTNVTIROPAAPAG------GGVITLHGRF 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DILSLIGTALPPPAPPGAGGLTVYLAGGQGQVVGGNVAGSLIASGPVVLMAASFANAVYD 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RLPIEEEETPPPRTTGVQQQPEASQSSEVTGSGAQACESNLQGGNGG------GG 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RLPLEDE------GGEGGEGGEV-GEGG------GGEGGPPPATSSSPPSG 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DEAKAETTPTGGATSSATASGSSSGRRPRGRPAGSKNKPKPPTIITRDSPNVLRSHVLEV 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        46.4%; Score 645.5; DB 10; Length 302;
llarity 49.5%; Pred. No. 7.2e-37;
Conservative 33; Mismatches 63; Indels 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11 protein.
302 AA; 30615 MW; 6EC755021E3DD375 CRC64;
                                                                                                                                                                   01.JUN-2001 (TrEMBLrel. 17, Created)
01.JUN-2001 (TrEMBLrel. 17, Last sequence update)
01.JUN-2001 (TrEMBLrel. 17, Last annotation update)
HYPOTHETICAL 30.6 KDA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         232 VAFYNLGMNMNNFQFSGGDIYGMSGGSGGGGGGTRPAF 270
                                                                                                                                         302 AA
                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mature 400:816-820(2000).

EMBL: AC015450: AAG51949.1; -.

InterPro: INTRO00637: AT_hook.

Ffam: PF02178: AT_hook: 1.

SMART: SM00384: AT_hook: 1.
                                245 QFSGGDIYGMSGGSGGG 262
                                                           276 QL---PVEGWPGNSGGRG 290
                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 138; Conserv
                                                                                                                                                                                                                                                                                                                            [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                           NCBI_TaxID-3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical
SEQUENCE 3(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   thaliana."
                                                                                                                                    Q9C9K7
Q9C9K7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 107
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                                                                                                       RESULT
                                                                                                                       Q9C9K7
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              243 AERGGGGGSGGVVPGQ-------LGGGGSPLSSGAGGGDGNQGLPVYNMPGNLVS--- 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     77 AVSTYATRRGCGVCIISGTGAVTNVTIRQP-----AAPAGGGVITLHGRFDILSLTGTA 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 191 PP----PRTTGVQQQQPEASQSSEVTGSGAQACESNLQGGNGGGGVAFYNLGMNNNFQF 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17 PTGGATSSATASGSSSGRRPRGRPAGSKNKPKPPTIITRDSPNVLRSHVLEVTSGSDISE 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN-CV. COLUMBIA;
Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B.,
Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B.,
Ronning C.M., Koo H., Fujii C.Y., Utterback T.R.,
Bowman C.L., White O., Nierman W.C., Fraser C.M.;
"Arabidopsis thaliana chromosome III BAC F7018 genomic sequence.",
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AC011437; AAF04888.1; -.
SEQUENCE 315 AA; 32037 MW; 1766141EC657C448 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                45.8%; Score 637.5; DB 10; Length 315; 50.0%; Pred. No. 2.7e-36; Live 37; Mismatches 58; Indels 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
                                                                                                                                                                                               Created)
Last sequence update)
Last annotation update)
265 AGGGOLRGNMSGYDQFAGDPH-LLGWGAAAAAPPRPAF 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  317 AA
                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PUTATIVE AT-HOOK DNA-BINDING PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-CV. COLUMBIA; MEDLINE-20083487; Pubmed-10617197;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       247 SGGDIYGMSGGSGGGGGGATRPAF 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    291 -----NGGSGGGQMSGQEAY 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (TrEMBLrel. 05, C
(TrEMBLrel. 05, I
(TrEMBLrel. 19, I
                                                                                                                                                                                            01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 50.0%
Matches 132; Conservative
                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
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                                                                                                                                                                                                                                                                        F7018.4 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=3702;
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01-DEC-2001
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                                                                                                                                                                       09SR17;
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                                                                                                RESULT
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Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D., Fujii. C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V., Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S., Cronin L.A., Shen M., VanAken S.E., Umayam L., Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M., Venter J.C.; the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
Bevan M., Hilbert H., Braun M., Holzer E., Brandt A., Duesterhoeft A.,
Bancroft I., Mewes H.W., Mayer K.F.X., Schueller C.;
Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thaliana (Mouse-ear cress).

Bukaryota, Viiddiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.

NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     115 ALKSHVMEVANGCDVMESVIVFARRRQRGICVLSGNGAVTNVTIRQPASVPGGGSSVVNL 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60 VLRSHVLEVTSGSDISEAVSTYATRRGCGVCIISGTGAVTNVTIRQPAAPAGGG--VITL 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            118 HGRFDILSLTGTALPPPAPPGAGGLTVYLAGGQGQVVGGNVAGSLIASGPVVLMAASFAN 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  55 DIDPNEHSSAGKDQSTPGSGGESGGGGGDNHITRRPRGRPAGSKNKPKPPIIITRDSAN 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 ELNRSEADEA-KAETTPTGGATSSATASGSSS-GRRPRGRPAGSKNKPKPPTIITRDSPN 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        178 AVYDRLPIEEEETPPPRTTGVQQQQPEASQSSEVTGSGAQACESNLQGGNGGG 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            235 AAYERLPLEEDD-----GEEQTAGAVANNIDGNATM-----GGG 268
                                                                                                                                                                                                                                                                                                                                                                                                                         DB 10; Length 317;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
Hilbert H., Braun M., Holzer E., Brandt A., Duesterhoeft A.,
Mewes H.W., Lemcke K., Mayer K.F.X.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                  Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AC002387; AAB82621.1; -.
DNA-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EU Arabidopsis sequencing project;
Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                 317 AA; 33519 MW; 3A3677B991AE25F0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-CCT-2000 (TrEMBLrel. 15, Last annotation update)
PUTATIVE DNA-BINDING PROTEIN.
F16J13.120 OR AT4G12050.
                                                                                                                                                                                                                                                                                                                                                                                                                     45.2%; Score 629.5; DB 10; 54.1%; Pred. No. 9.5e-36; Live 37; Mismatches 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             339 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAY-2000 (TrEMBLrel. 13, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Best_Local Similarity 54.1%
Matches 126; Conservative
                                                                                                                                                                                                          Nature 402:761-768(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. STRAIN=CV. COLUMBIA;
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                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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                                                                                                                                                                                                                                                                                          Lin X.,
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STRAIN—CV. COLUMBIA;

MEDLINB=20083487; PubMed=10617197;

Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,

Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,

Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,

Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,

Cronin L.A., Shen M., VanAken S.E., Umayam L., Tallon L.J., Gill J.E.,

Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,

Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,

Salzberg S.L., Fraser C.M., Venter J.C.;

"Sequence and analysis of chromosome 2 of the plant Arabidopsis

thallana."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              184 PIEEEETPPPRTTGVQQQQPEASQSSEVTGSGAQACESNLQGGNGGGGVAFYNLGMNMNN 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    267 PLEEDEMQTP------ 285
                                                                                                                                                                                                                                                                                                                                                                                                              88 NTNSGSEGKEMSLHGGEGGSGGGGGGGGGQMTRRPRGRPAGSKNKPKAPIIITRDSANALRT 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64 HVLEVTSGSDISEAVSTYATRRGCGVCIISGTGAVTNVTIRQPAAPAGGGVITLHGRFDI 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                             4 NRSEADEAKAETTPTGGATSSATASGSSSGRRPRGRPAGSKNKPKPPTIITRDSPNVLRS 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           124 LSLTGTALPPPAPPGAGGLTVYLAGGQGQVVGGNVAGSLIASGPVVLMAASFANAVYDRL
                                                                                                                                                                                                                                                                            57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          38;
                                                                                                                                                                                                   44.9%; Score 625.5; DB 10; Length 339; 49.2%; Pred. No. 1.9e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match

44.3%; Score 616; DB 10; Length 285;
Best Local Similarity 49.6%; Pred. No. 7.1e-35;
Matches 130; Conservative 30; Mismatches 64; Indels 36
                                                                                                                                                                                                                                                                            48; Indels
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                                                                                                 339 AA; 35785 MW; A7E3A9C73B6BBE21 CRC64;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                244 FQFSGGDIYGMSGGSGGGGGA 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  286 ------GGGGMGS 292
EMBL; AL049638; CAB40946.1; -. EMBL; AL161533; CAB78248.1; -. DNA-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1998 (TrEMBLrel, 08, 01-NOV-1998 (TrEMBLrel, 08,
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                                                                                                                                                                                                              Query Match

Best Local Similarity 49.29
Matches 129; Conservative
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Bancroft I., Mewes H.W., Mayer K., Schueller C.;
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
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                          :|: |||||||||| ||::||| ||||||||||| ||::||||| ||:||||:
SGSFLPPPAPPGATSLTIFLAGAQGQVVGGNVVGELMAAGPVMVMAASFTNVAYERLPLD 228
                                                                                                                                                                                                                                                                                                        EVTSGSDISEAVSTYATRRGCGVCIISGTGAVTNVTIRQPAAPAGGGVITLHGRFDILSL 126
                                                                                                                                                                                     127 TGTALPPPAPPGAGGLTVYLAGGQGQVVGGNVAGSLIASGPVVLMAASFANAVYDRLPIE 186
                                                                                                                                                                                                                                                                              EEETPPPRITGVQQQPEASQSSEVIGSGAQACESNLQGGNGGGGVAFYNLGMNMNNFQF 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arabidopsis thallana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11 AKAETTPTGGATSSATASGSSSG----RRPRGRPAGSKNKPKPPTIITRDSPNVLRSHVL
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Hilbert H., Braun M., Holzer E., Brandt A., Duesterhoeft
Mewes H.W., Lemcke K., Mayer K.F.X.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
EMBL; ALO21635; CAA16566.1; -.
EMBL; ALI61558; CABA70236.1; -.
SEQUENCE 324 AA; 34339 MW; B8EF7520B474C528 CRC64;
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Matches 129; Conserv
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           154 VGGNVAGSLIASGPVVLMAASFANAVYDRLPIEEEETPPPRTTGVQQQQPEASQSSEVTG 213
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Benes V., Wurmbach E., Drzonek H., Ansorge W., Mewes H.W., Lemcke K.,
Mayer K.F.X., Quetler F., Salanoubat M.;
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               57; Indels 30; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34 RRPRGRPAGSKNKPKPPTIITRDSPNVLRSHVLEVTSGSDISEAVSTYATRRGCGVCIIS 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  214 SGAQACESNLQGGNGGGGVAFYNLGMNMNNFQFSGGDIYGMSGGSGGGGGGATRPAF 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                219 NAARAIGTQTQKQLMQDATSFIGSPSNLINSVSLPGEAY------WGTQRPSF 265
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
Cholsne N., Robert C., Brottier P., Wincker P., Cattolico L. Artiguenave F., Saurin W., Welssenbach J., Mewes H.W., Rudd Lemoke K., Mayer K.F.X., Quetier F., Salanoubat M.; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 265;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AL162295; CABB2691.1; -.
Hypothetical protein.
SEQUENCE 265 AA; 28412 MW; 31162D06E4BAD0AD CRC64;
                                                                                                                      01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
HYPOTHETICAL 32.6 KDA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41.7%; Score 581; DB 10;
50.2%; Pred. No. 1.6e-32;
11ve 31; Mismatches 57;
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Arabidopsis thaliana (Mouse-ear cress).
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                                                                                                                                                                                                                      HYPOTHETICAL 28.4 KDA PROTEIN
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Best Local Similarity 50.2%
Matches 119; Conservative
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                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=3702;
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                                                                                         09LZX7;
                                                              09L2X7
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RESULT 10
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Best Local Similarity
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Q9LTA2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lin X., Kaul S., Rounaley S.D., Shea T.P., Benito M.-I., Town C.D., Fujii C.Y. Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V., Buelli C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S., Cronin L.A., Shen M., VanAken S.E., Umayam L., Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R., Copenhaver G.P., Preseus D., Nierman W.C., White O., Eisen J.A., Salzberg S.L., Fraeus C.M., Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana (Mouse-ear cress).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
                                                                                                                                                                   119 VLEIATGADVAESLNAFARRRGRGVSVLSGSGLVTNVTLRQPA--ASGGVVSLRGQFEIL 176
                                                                                                                                                                                                                                                             SLIGTALPPP-APPGAGGLTVYLAGGQGQVVGGNVAGSLIASGPVVLMAASFANAVYDRL 183
                                                                                                                                                                                                                                                                                                                  PIEEEETPPPRTTGVQQQPEASQSSEVTGSGAQACESNLQGGNGGGGVAFYNLGMNM-- 241
                                                                                                                                                                                                        VLEVTSGSDISEAVSTYATRRGCGVCIISGTGAVTNVTIRQPAAPAGGGVITLHGRFDIL 124
                                                                                                                                                                                                                                                                                                                                            237 PIEEEQ------QOEQPLQLEDGKKOKEENDDNESGNNGNEGSMQPPMYNMPPNFIP 287
                                                                                                                                                   5 RSEADEAKAETTPTGGATSSATASGSSSGRRPRGRPAGSKNKPKPPTIITRDSPNVLRSH 64
                                                                                                                                                                                                                                                                           41.1%; Score 572; DB 10; Length 310;
47.8%; Pred. No. 8e-32;
Live 44; Mismatches 69; Indels 18
               the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EU Arabidopsis sequencing project;
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ database:
EMBL, AL132975, CAB75914.1; -.
Hypothetical protein.
SEQUENCE 310 AA; 32603 MW; 0F856170E37A40CB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       00DA8F50213F6DE9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   257 AA.
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MEDLINE-20083487; PubMed=10617197;
                                                                                                                        44;
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InterPro; IPR000637; AT_hook.
Pfam; PF02178; AT_hook; 1.
SMART; SM03384; AT_hook; 1.
SEQUENCE 257 AA; 27004 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY 2000 (TrEMBLrel. 13, 01-MAY 2000 (TrEMBLrel. 13, 01-DEC-2001 (TrEMBLrel. 19, AT2G42940 PROTEIN.
                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature 402:761-768(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
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288 NGHQMAQHDVY 298
                                                                                                                                                                                                                                                                                                                                                                       242 NNFQFSGGDIY 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-CV. COLUMBIA;
                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   [1]
SEQUENCE FROM N.A.
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                                                                                                              Best Local Sin
Matches 120;
                                                                                               Query Match
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Length 257;

Score 554; DB 10;

39.8%;

*Qmerji Match

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Eukaryota; Viidiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                         49 PPTIITRDSPNVLRSHVLEVTSGSDISEAVSTYATRRGCGVCIISGTGAVTNVTIRQPAA 108
                                                                                                                                                                                        135 -APPGAGGLTVYLAGGQQQVVCGNVAGSLIASGPVVLMAASFANAVYDRLPIEEETPPP 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       194 RTTGVQQQQPEAS----QSSEVTGSGAQACESNLQGGNGGGGVAFYNLGMNMNFQFSGG 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      79 STYATRRGCGVCIISGTGAVTNVTIRQPAAPAGGGVITLHGRFDILSLTGTALPPP---- 134
                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                  16 TPTGGATSS-----ATASGSSS-----ATASGSSS------GRRPRGRPAGSKNKPK 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21 ATSSATASGSSSG--RRPRGRPAGSKNKPRPPTIITRDSPNVLRSHVLEVTSGSDISEAV 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           221 GTGEREGQSPPVSGGGEESGQMAGSGGESC-----GVSMYSCHM------GGS
                                                                                                                                                                                                                                                      109 PAGGGVITLHGRFDILSLTGTALPPPAPPGAGGLTVYLAGGQGQVVGGNVAGSLIASGPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-COLUMBIA;
Kaneko T., Katoh T., Asamizu E., Sato S., Nakamura Y., Kotani H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5. XI.";
                       34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              35.9%; Score 499.5; DB 10; Length 276; 43.8%; Pred. No. 6.5e-27;
                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Structural analysis of Arabidopsis thallana chromosome Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases. EMBL; AB025613; BAA98158.1; ...
DNA-binding.
SEQUENCE 276 AA; 29390 MW; A804D55ADA0568BF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99
  Pred. No. 1.1e-30;
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                                                                                                                                                                                                                                                                                                                                                                                         186 VLMAASFMNAVFDRLPMDDDE----AASMQNQQ 214
                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence v
01-0CT-2000 (TrEMBLrel. 15, Last annotation
SIMILARITY TO AT-HOOK DNA-BINDING PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                              169 VLMAASFANAVYDRLPIEEEETPPPRTTGVQQQQ
                       30;
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52.8%;
                       Matches 113; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           106; Conservative
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Best Local Similarity
Matches 106; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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Q9M9R4
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Liu S., Sakano H., Yu G., Lee J., Lenz C., Pham P., Toriumi M.,
Chiu S., Chiou J., Choi E., Ching M., Gonzalez A., Howng B., Liu A.,
Vaysberg M., Altefi H., Brooks S., Buehler E., Chao Q., Conn L.,
Conway A., Hansen N., Johnson-Hopson C., Khan S., Kim C., Lam B.,
Miranda M., Nguyen M., Palm C., Shinn P., Southwick A., Davis R.,
Ecker J., Federspiel N., Theologis A.;
"The sequence of BAC F14L17 from Arabidopsis thaliana chromosome 1.";
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                         Arabidopsis thallana (Mouse-ear cress).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95 TGAVTNVTIRQPAAPAGGGVITLHGRFDILSLTGTALPP-----PAPPGAGGLTVYLAGG 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                150 QGQVVGGNVAGSLIASGPVVLMAASFANAVYDRLPIEEEETPPPRTTGVQQQPEASQSS 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59; Indels 16; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 35 RPRGRPAGSKNKPKPPTIITRDSPNVLRSHVLEVTSGSDISEAVSTYATRRGCGVCIISG 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oryza sativa (Rice).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Lillopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30.0%; Score 417; DB 10; Length 206; 46.0%; Pred. No. 2.1e-21; tive 32; Mismatches 59; Indels 1
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Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases. EMBL; AC012188; AAF43950.1; -... Interpret; IPR000637; AT_hook. SMART; SMO384; AT_hook; 1. SEQUENCE 206 AA; 21459 MW; CE20976A467287C8 CRC64;
          01-0cT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
F14L17.27 PROFEIN.
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Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              91; Conservative
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                                                                                                                                                             NCBI_TaxID=3702;
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                                                                              F14L17.27
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Matches
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184 PIEEEETPPPRTTGVQQQQPEASQSSEVTGSGAQACESNLQGGNGGGGVAFYNLGMNMNN 243
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             178 PADEDDEATGSRGGEERRHPQ--QQPPQTVAATSAVDVGLLGYGGGVGVA----- 225
                                                                                                                                                                                                                           13 EASPAPALDLP-----SPPRKPRGRPLGSKNKPKPRPPVVVTRESEAAMRPVVL 59
                                                                                                                                                                    Gaps
                                                                                                                                                                                                  7 EADEAKAETTPTGGATSSATASGSSSGRRPRGRPAGSKNKPKPPTITTRDSPNVLRSHVL 66
                                                                                                                                                                42;
                                                                                                                    29.2%; Score 407; DB 10; Length 265; 36.8%; Pred. No. 1.3e-20; tive 40; Mismatches 83; Indels 4.
clone:P0431G06.";
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AP003683; BAB64709.1; -.
SEQUENCE 265 AA; 26638 WW; 1BB4ED3E30AD6CAA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Search completed: July 10, 2002, 22:28:40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     244 FQFSGGDIYGMSGGSGGGGG 264
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                                                                                                                                                              Conservative
                                                                                                              Ouery Match
Best Local Similarity
Matches 96; Conserv?
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